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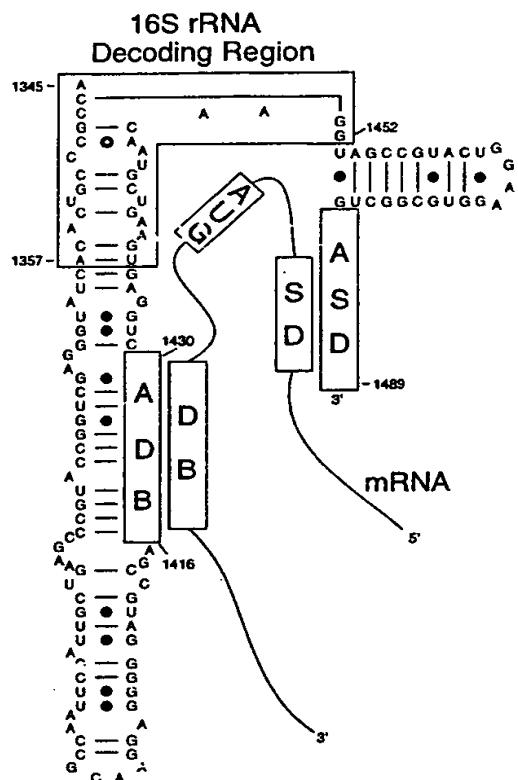


Figure 1A

1 10 20 26

pt ADB 3' - AGGUCAGUGAUCGGGACGGAAGCCGU-5'

1430 1416

1 10 20 26

Ec ADB 3' - GGGUCAGUACUUAGUGUUUCACCAUU-5'

1483 1469

Figure 1B

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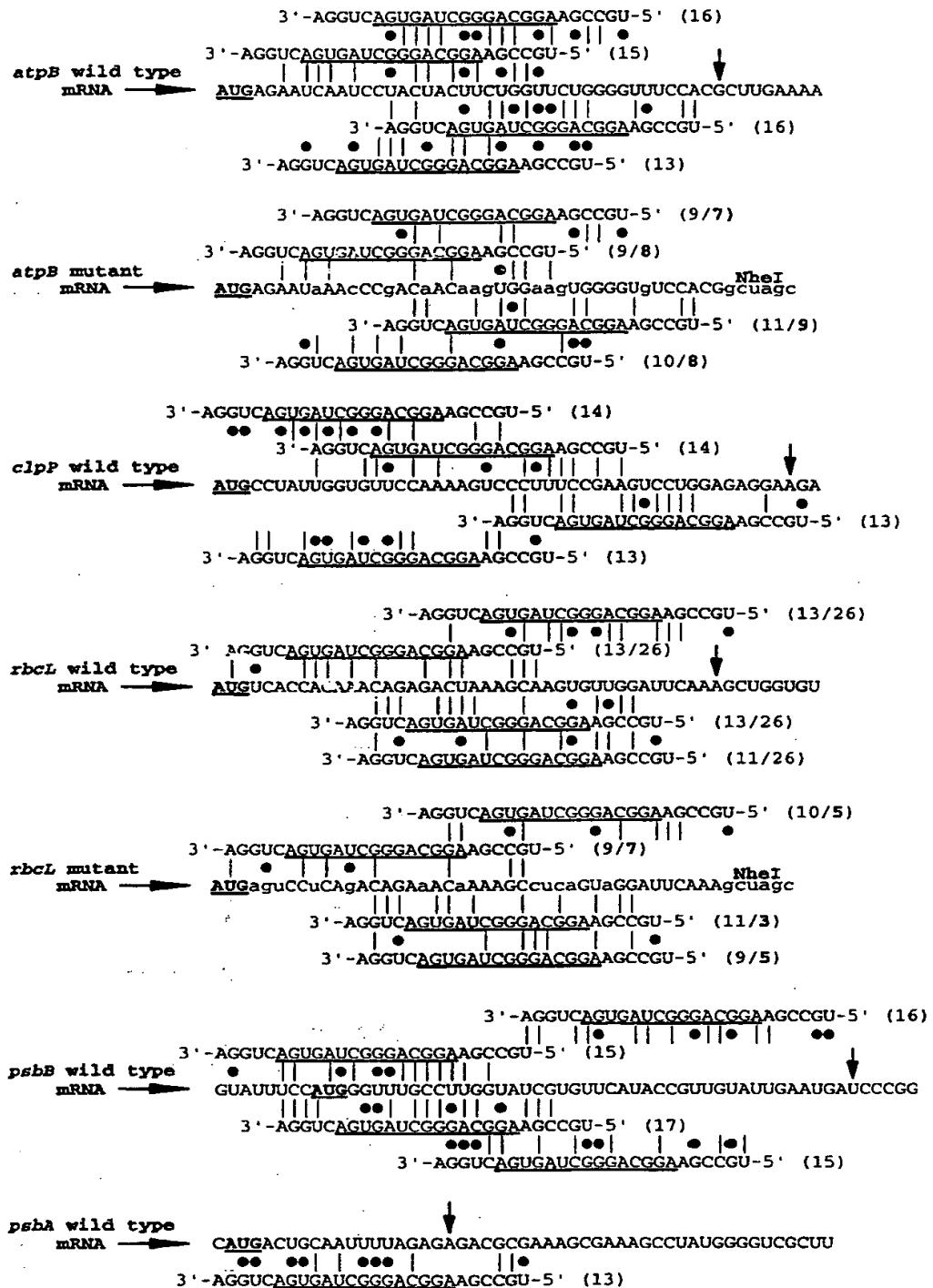


Figure 2A

T7g10 mRNA AUGGCUAGCAUGACUGGUGGACAGCAAUGGUCGCCAUCCGGCUGCUA
Ec ADB 3'-GGGUCAGUACUUAGUGUUCACCAUU-5' (15)

T7g10+DB/Ec mRNA AUGGCaAGCAUGACUGGUGGACAGggcuagc
pt ADB 3'-AGGUCAGUGAUCGGGACCGGAAGCCGU-5' (13)

T7g10+DB/pt mRNA AUGGCaAucacuagcccugccuuGgcuagc
pt ADB 3'-AGGUCAGUGAUCGGGACCGGAAGCCGU-5' (21)

T7g10-DB mRNA ACAUAVGgcuaagcauugaacaagauggauugcau
pt ADB 3'-AGGUCAGUGAUCGGGACCGGAAGCCGU-5' (14)

Figure 2B

PrrnLatpB+DBwt (pHK10)

SacI

1 gagctcGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGca AGCGGACATT TATTTTaAAT TCGATAATTT TTGCAAAAAC
 151 ATTTCGACAT ATTTATTAT TTTATTATTA TGAGAATCAA TCCTACTACT
 NheI
 201 TCTGGTTCTG GGGTTTCCAC Ggctagc

PrrnLatpB-DB (pHK11)

SacI

1 gagctcGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGca AGCGGACATT TATTTTaAAT TCGATAATTT TTGCAAAAAC
 151 ATTTCGACAT ATTTATTAT TTTATTATTA TGAGAgctag c
 NheI

PrrnLatpB+DBm (pHK50)

SacI

1 gagctcGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGca AGCGGACATT TATTTTaAAT TCGATAATTT TTGCAAAAAC
 151 ATTTCGACAT ATTTATTAT TTTATTATTA TGAGAATaAA cCCgACaACa
 NheI
 201 agTGGaaagTG GGGTgTCCAC Ggctagc

PrrnLclpP+DBwt (pHK12)

SacI

1 gagctcGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TTACGTTCC
 101 ACCTCAAAGT GAAATATAGT ATTTAGTTCT TTCTTTCATT TAATGCCTAT
 NheI
 151 TGGTGTTCCCA AAAGTCCCTT TCCGAAGTCC TGGAGAGGAA gctagc

PrrnLclpP-DB (pHK13)

SacI

1 gagctcGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TTACGTTCC
 NheI
 101 ACCTCAAAGT GAAATATAGT ATTTAGTTCT TTCTTTCATT TAATGCCTgc
 151 tagc

Figure 3A

PrrnLrbcl+DBwt (pHK14)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
 101 CTTGTTGTTG TGAAATTCT TAATTCATGA GTTGTAGGGA GGGATTATG
 151 TCACCACAAA CAGAGACTAA AGCAAGTGTT GGATTCAAAg ctac

NheI

PrrnLrbcl-DB (pHK15)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
 101 CTTGTTGTTG TGAAATTCT TAATTCATGA GTTGTAGGGA GGGATTATG
 151 TCAGcttagc

NheI

PrrnLrbcl+DBm (pHK54)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
 101 CTTGTTGTTG TGAAATTCT TAATTCATGA GTTGTAGGGA GGGATTATG
 151 aguCCuCAGA CAGAAACAA AGCcucAGTa GGATTCAAAg ctac

NheI

PrrnLpsbB+DBwt (pHK16)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
 101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTCCATGGGT
 151 TTGCCCTGGT ATCGTGTCA TACCGTTGTA TTGAATGATg ctac

NheI

PrrnLpsbB-DB (pHK17)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
 101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTccatggct
 151 agc

NcoI

NheI

Figure 3B

PrrnLpsbA+DBwt (pHK21)

SacI
1 gagctcGCTC CCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
101 CATTCTAT TTTGATTGT AGAAAATAG TGTGCTTGGG AGTCCCTGAT NheI
151 GATTAAATAA ACCAAGATT TACCATGACT GCAATTAG AGAGAgctag
201 c

PrrnLpsbA-DB (pHK22)

SacI
1 gagctcGCTC CCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
101 CATTCTAT TTTGATTGT AGAAAATAG TGTGCTTGGG AGTCCCTGAT NcoI NheI
151 GATTAAATAA ACCAAGATT TAccatggct agc

PrrnLpsbA-DB(+GC) (pHK23)

SacI
1 gagctcGCTC CCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAAAAAGCCT
101 TCCATTCT ATTTGATT GTAGAAAAT AGTGTGCTTG GGAGTCCCTG NcoI NheI
151 ATGATTAAAT AACCAAGAT TTTAccatgg cttagc

Figure 3C

PrrnLT7g10+DB/Ec (pHK18)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
151 ATATGGCaAG CATGACTGGT GGACAGgcta gc

PrrnLT7g10+DB/pt (pHK19)

SacI

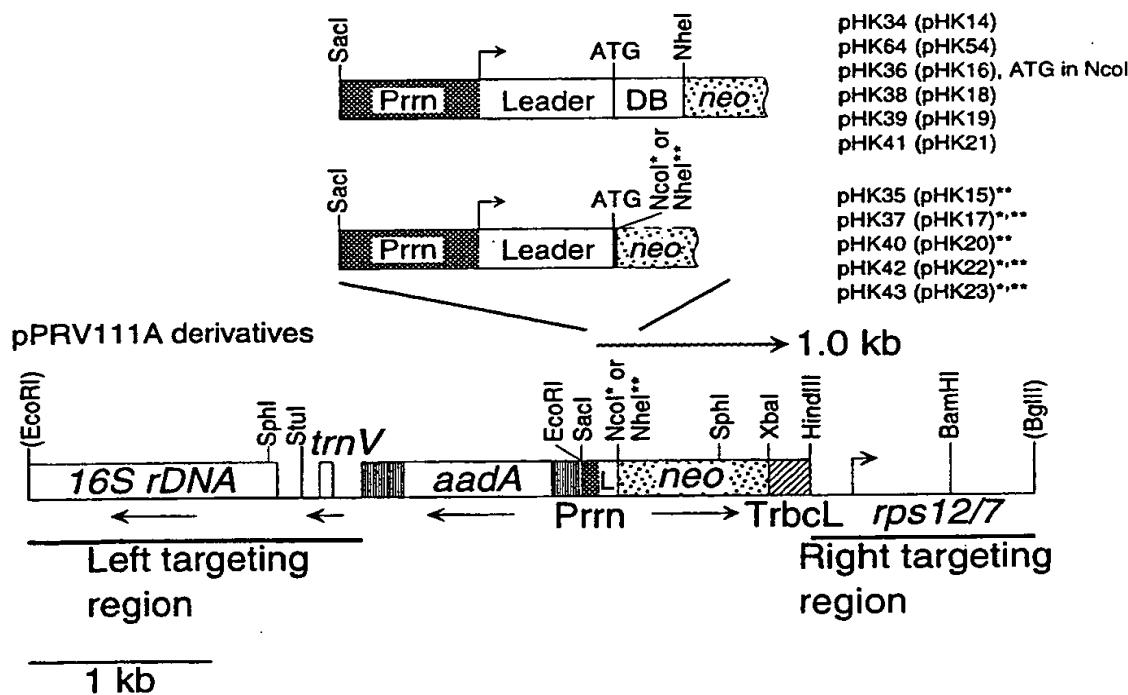
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51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
151 ATATGGCaAt cactagccct gccttGgcta gc

PrrnLT7g10-DB (pHK20)

SacI

1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
151 ATATGgctag c

Figure 3D

**Figure 4A**

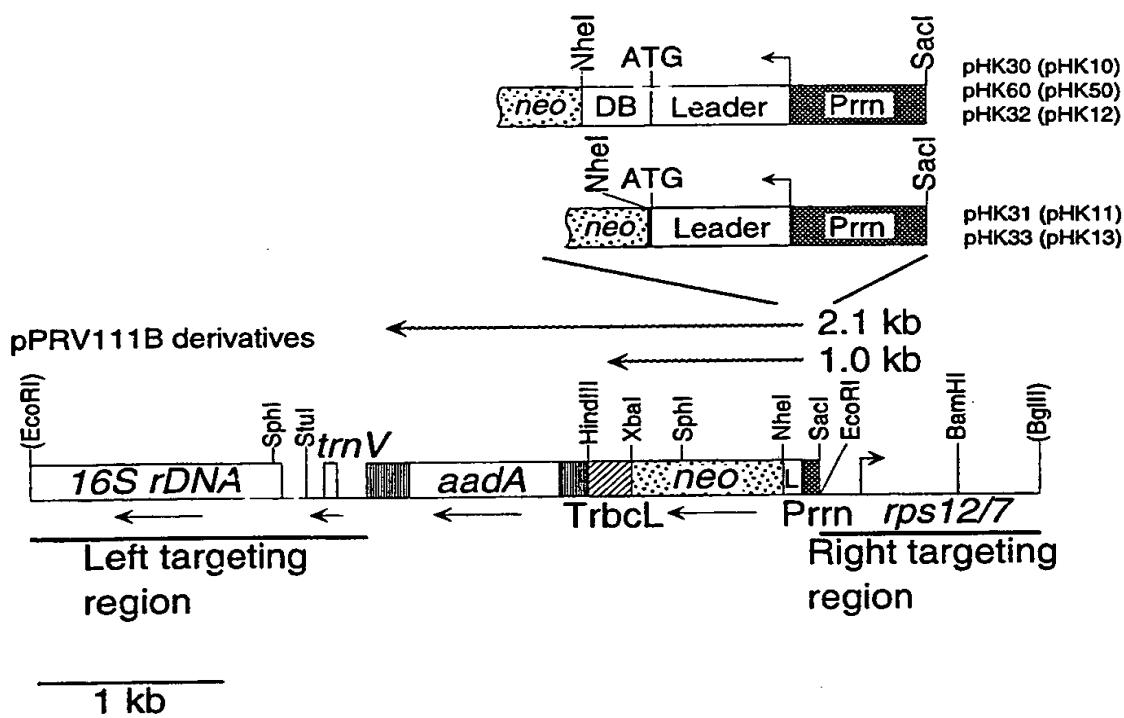
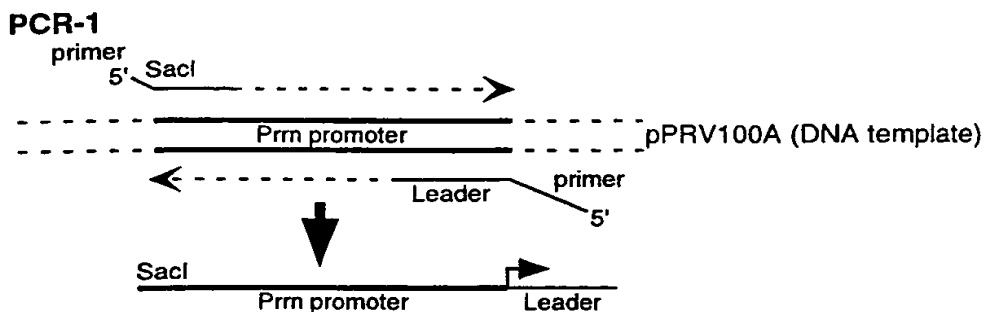
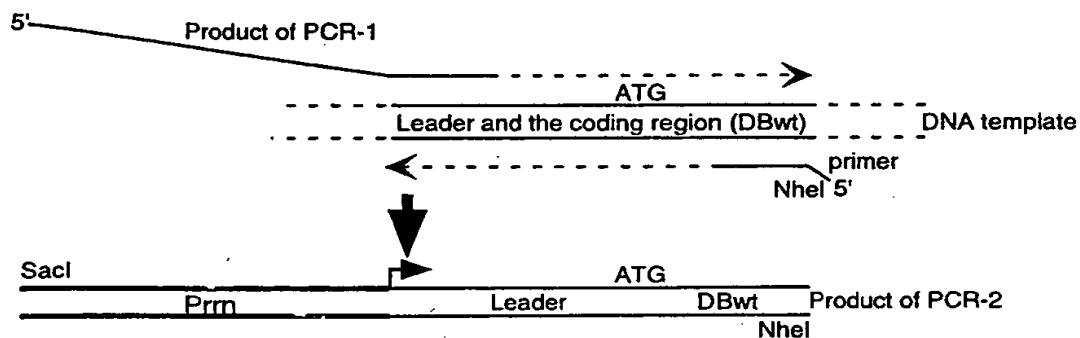


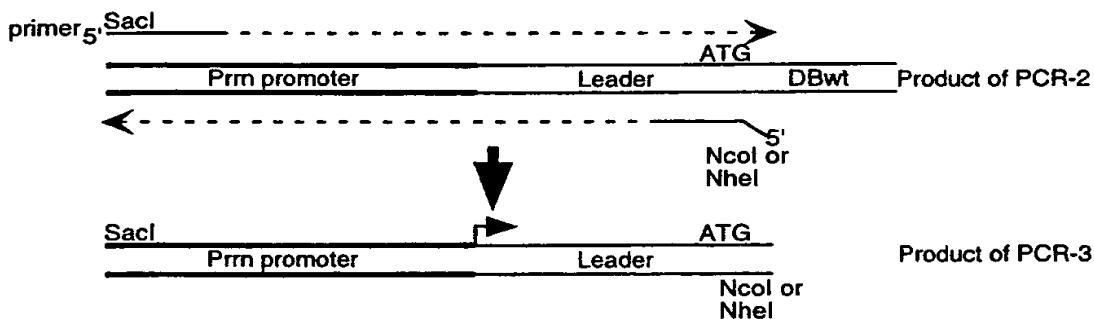
Figure 4B



PCR-2: Construct with wild-type DB (DBwt)



PCR-3: Construct without DB



PCR-4: Construct with mutant DB (DBm)

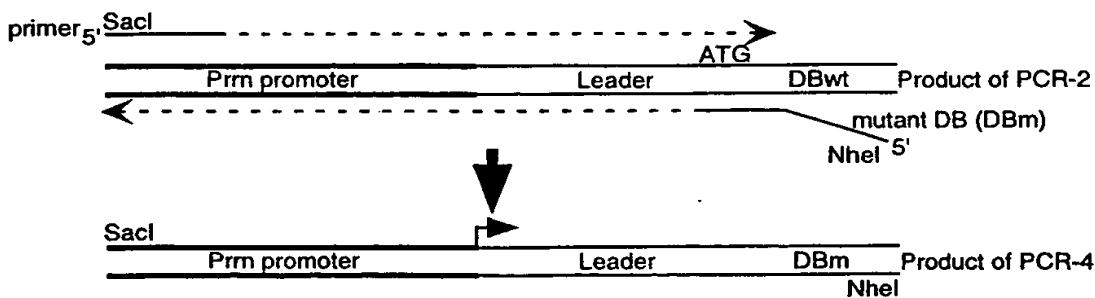
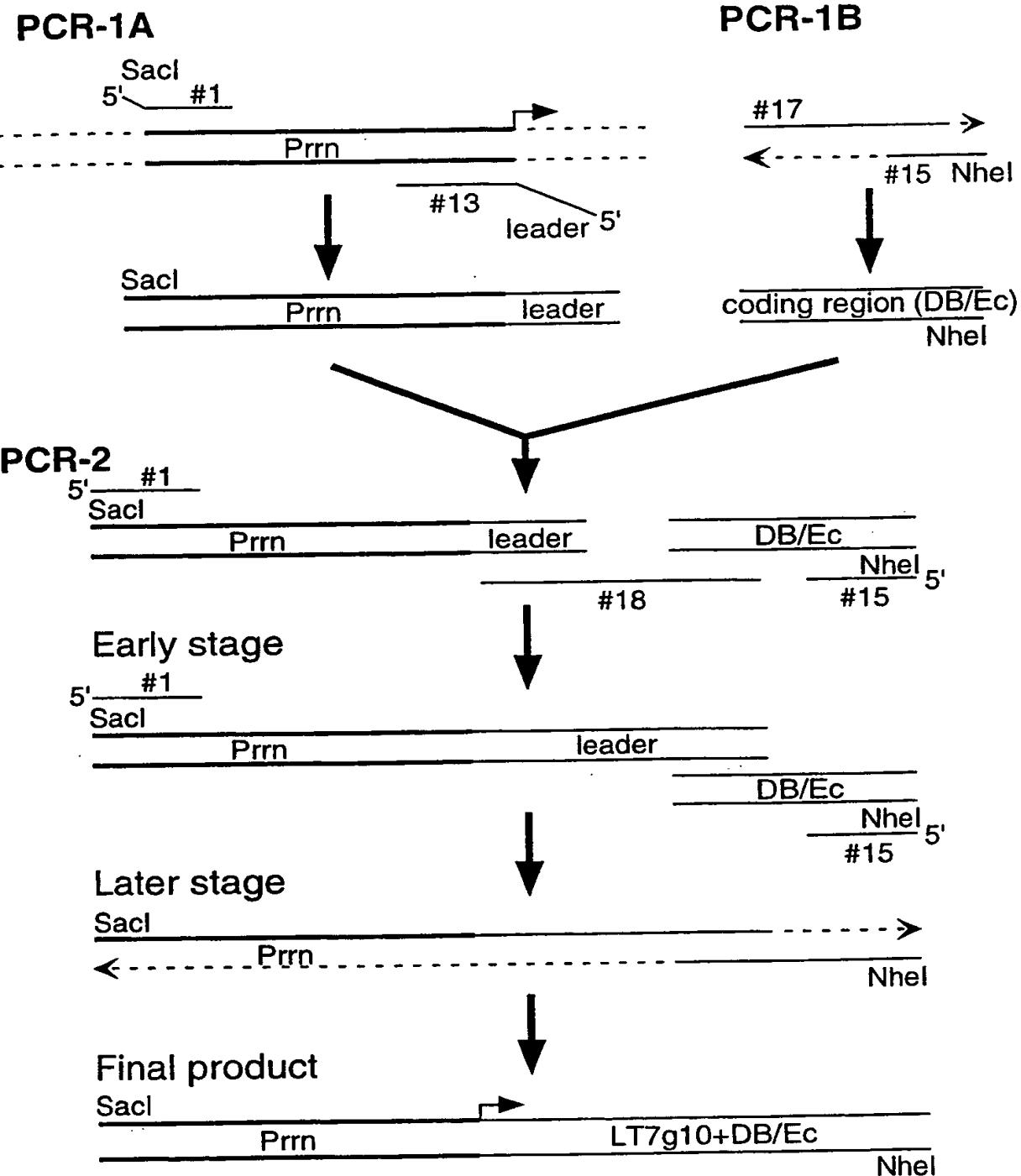


Figure 5

**Figure 6**

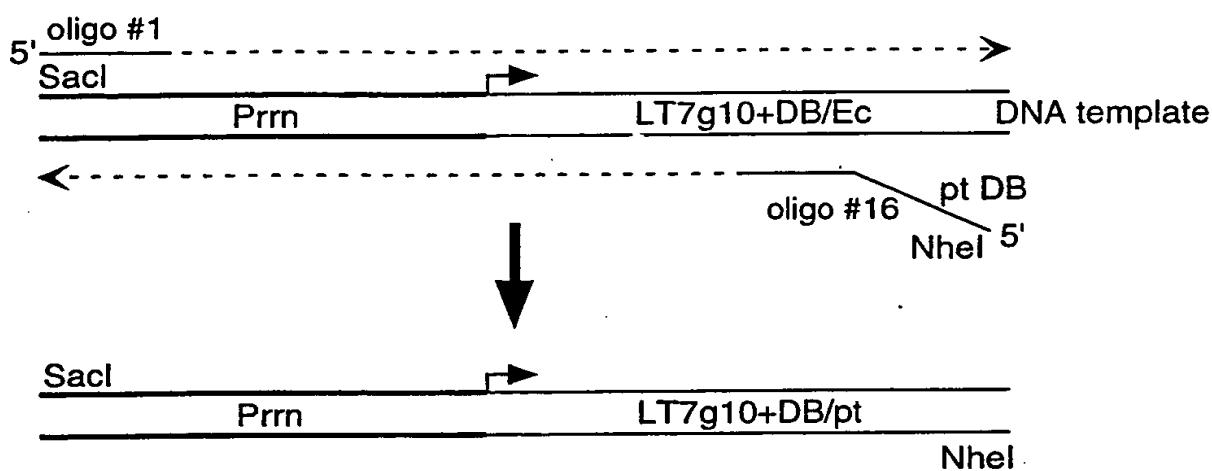


Figure 7

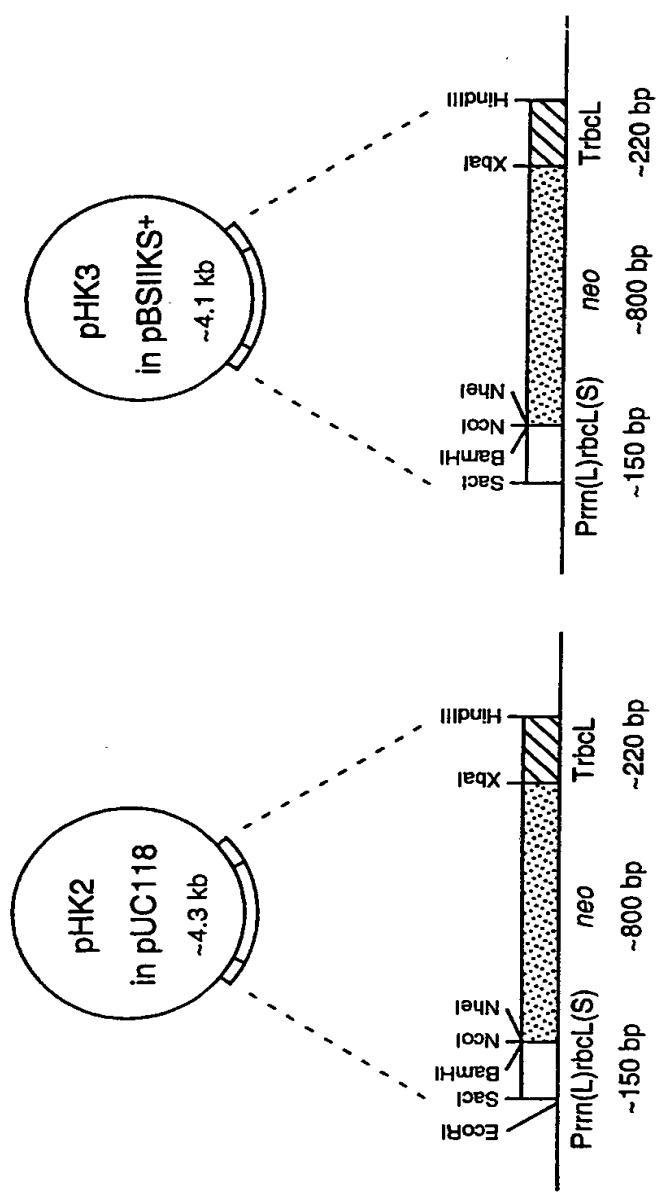


Figure 8

SacI

1 gagctcggt a cccaaaGCTC CCCCCGCCGTC GTTCAATGAG AATGGATAAG

51 AGGCTCGTGG GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG

101 CGAACTCCGG GCGAATACGA AGCGCTTGGA TACAGTTGTA GGGAGGGATc
NcoI

151 catggcttagc ATTGAACAAG ATGGATTGCA CGCAGGTTCT CGGGCCGCTT

201 GGGTGGAGAG GCTATTGGC TATGACTGGG CACAACAGAC AATCGGCTGC

251 TCTGATGCCG CCGTGTCCG GCTGTCAGCG CAGGGCGCC CGGTTCTTT

301 TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAACCTCCAG GACGAGGCAG

351 CGCGGCTATC GTGGCTGGCC ACGACGGCGC TTCCCTGCGC AGCTGTGCTC

401 GACGTTGTCA CTGAAGCGGG AAGGGACTGG CTGCTATTGG GCGAAGTGCC

451 GGGGCAGGAT CTCCTGTCAT CTCACCTTGC TCCTGCCGAG AAAGTATCCA

501 TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC

551 CCATTGACCC ACCAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT

601 GGAAGCCGGT CTTGTCGATC AGGATGATCT GGACGAAGAG CATCAGGGC

651 TCGGCCAGC CGAACTGTTG GCCAGGCTCA AGGCGCGCAT GCCCGACGGC

701 GAGGATCTCG TCGTGACACA TGGCGATGCC TGCTTGCCGA ATATCATGGT

751 GGAAAATGGC CGCTTTCTG GATTCATCGA CTGTGGCCGG CTGGGTGTGG

801 CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT TGCTGAAGAG

851 CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTACG GTATCGCCGC

901 TCCCGATTTCG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTCT
XbaI

951 GAgcgggtct aqagtAGACA TTAGCAGATA ATTAGCAGG AAATAAAGAA

1001 GGATAAGGAG AAAGAACTCA AGTAATTATC CTTCGTTCTC TTAATTGAAT

1051 TGCAATTAAA CTCGGCCCAA TCTTTACTA AAAGGATTGA GCCGAATACA

1101 ACAAAAGATTC TATTGCATAT ATTTTGACTA AGTATATACT TACCTAGATA
HindIII

1151 TACAAGATTT GAAATACAAA ATCTAGcaag ctt

Figure 9

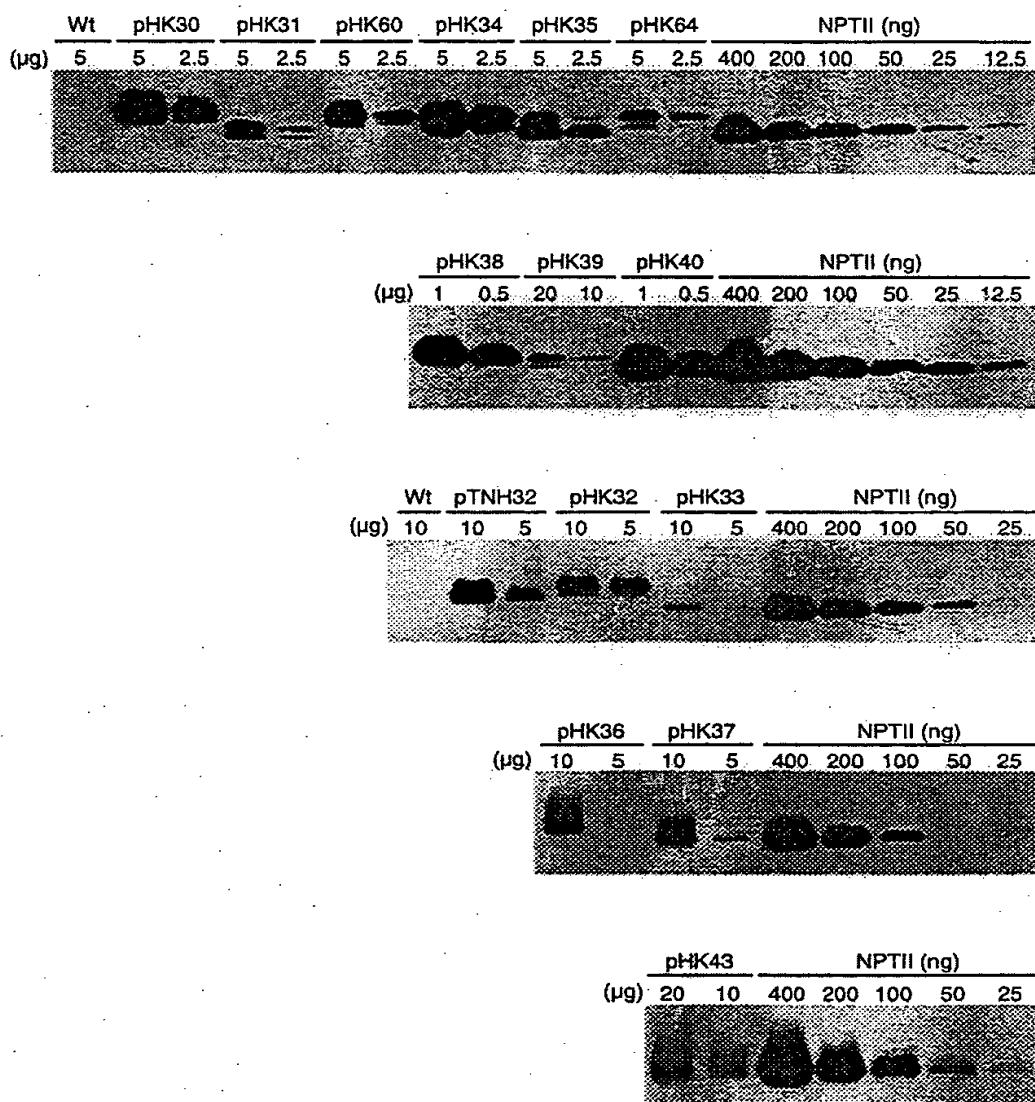


Figure 10

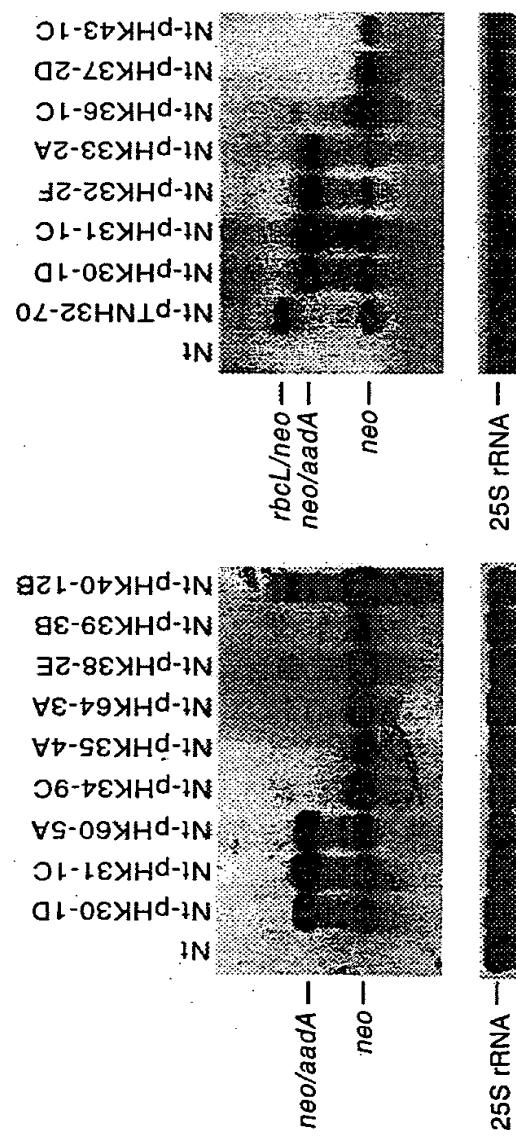


Figure 11

		AUG	AGA	AUC	AAU	CCU	ACU	UCU	GGU	GUU	UCC	ACG
		Met	Arg	Ile	Asn	Pro	Thr	Ser	Gly	Ser	Val	Thr
Fraction		1.0	0.22	0.27	0.61	0.30	0.37	0.31	0.38	0.31	0.26	0.14
Triplet/1000		24.6	7.8	15.5	18.1	13.5	18.4	18.4	20.2	28.2	20.2	24.9

		AUG	AGA	AUA	AAC	CCG	ACA	AGU	GGA	GGG	GUU	ACG
		Met	Arg	Ile	Asn	Pro	Thr	Ser	Gly	Ser	Val	Thr
Fraction		1.0	0.22	0.29	0.39	0.30	0.23	0.23	0.14	0.24	0.14	0.15
Triplet/1000		24.6	7.8	16.6	11.4	13.2	11.7	11.7	9.3	17.9	9.3	15.3

		AUG	UCA	CCA	CAA	ACA	GAG	ACU	AAA	GCA	AGU	GGU	GGA	UUC	AAA
		Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys
Fraction		1.0	0.21	0.24	0.57	0.23	0.38	0.37	0.60	0.29	0.14	0.35	0.24	0.40	0.60
Triplet/1000		24.6	13.5	10.6	21.0	11.7	12.4	18.4	22.0	18.1	9.3	24.9	17.9	22.5	22.0

		AUG	agu	CCU	CAG	ACA	GAA	ACA	AAA	GCC	uca	GUa	GGA	UUC	AAA
		Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys
Fraction		1.0	0.14	0.30	0.43	0.23	0.62	0.23	0.60	0.16	0.21	0.31	0.24	0.40	0.60
Triplet/1000		24.6	9.3	13.5	15.5	11.7	20.7	11.7	22.0	10.1	13.5	21.8	17.9	22.5	22.0

		AUG	GCA	AGC	AUG	ACU	GGU	GGA	CAG	gcu	agc	auu	gaa	caa	gau
		Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Ala	Ser	Ile	Glu	Gln	Asp
Fraction		1.0	0.29	0.07	1.00	0.37	0.37	0.38	0.24	0.43	0.39	0.07	0.45	0.62	0.57
Triplet/1000		24.6	18.1	4.7	24.6	18.4	28.2	17.9	15.5	24.4	4.7	25.9	20.7	21.0	24.6

		AUG	GCA	Auc	agc	ccu	gcc	uuG	gcu	agc	auu	gaa	caa	gau	
		Met	Ala	Ile	Thr	Ser	Pro	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Asp
Fraction		1.0	0.29	0.27	0.37	0.07	0.30	0.16	0.24	0.39	0.07	0.45	0.62	0.57	0.75
Triplet/1000		24.6	18.1	15.5	18.4	4.7	13.5	10.1	34.7	24.4	4.7	25.9	20.7	21.0	24.6

		AUG	gcu	agc	auu	gaa	caa	gau	gga	uug	cac	gca	ggu	ucu	ccg
		Met	Ala	Ser	Ile	Glu	Gln	Asp	Gly	Leu	His	Ala	Gly	Ser	Pro
Fraction		1.0	0.39	0.07	0.45	0.62	0.57	0.75	0.24	0.24	0.28	0.29	0.38	0.31	0.30
Triplet/1000		24.6	24.4	4.7	25.9	20.7	21.0	24.6	17.9	34.7	9.1	18.1	28.2	20.2	13.2

Figure 12

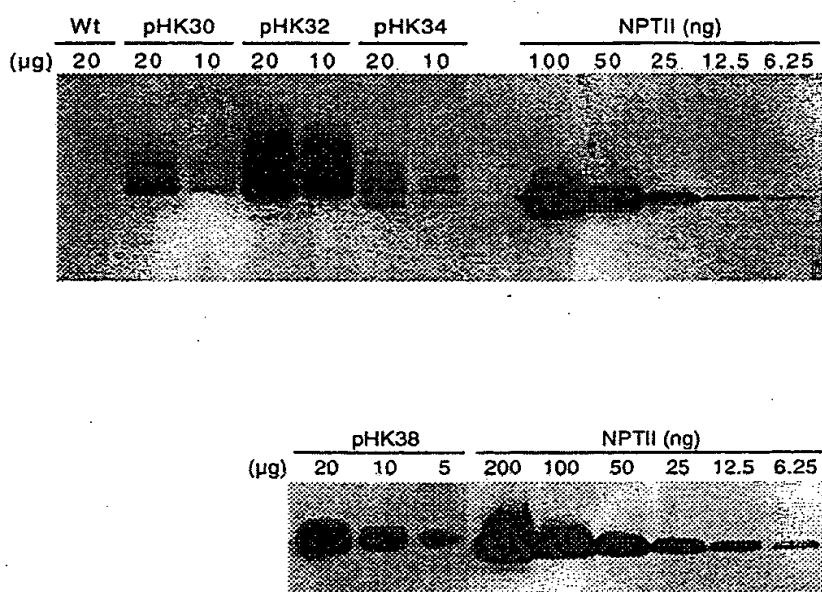


Figure 13A

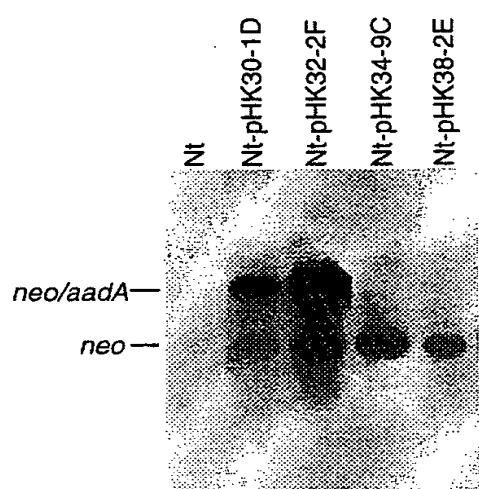


Figure 13B

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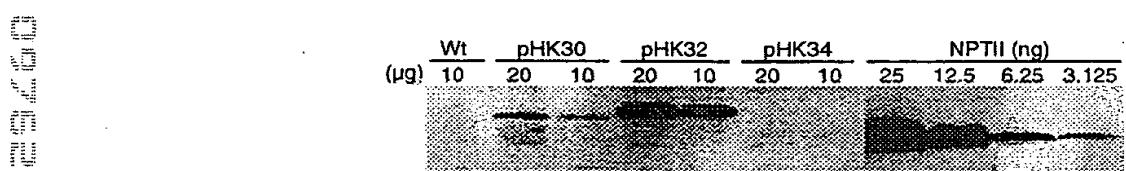


Figure 14

plasmids pHK30 and pHK32

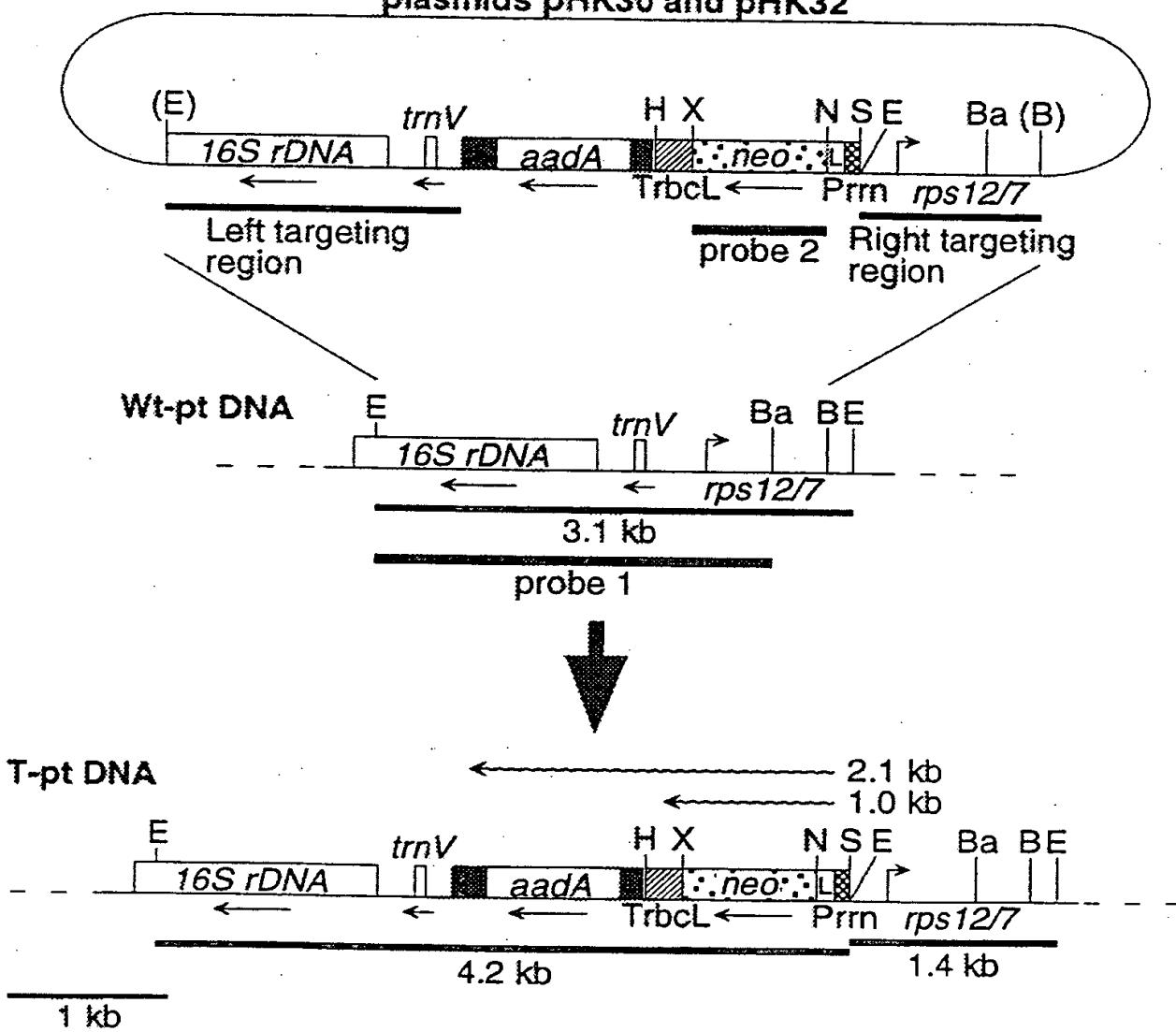


Figure 15A

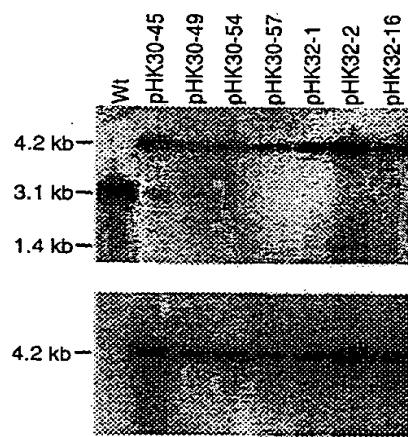


Figure 15B

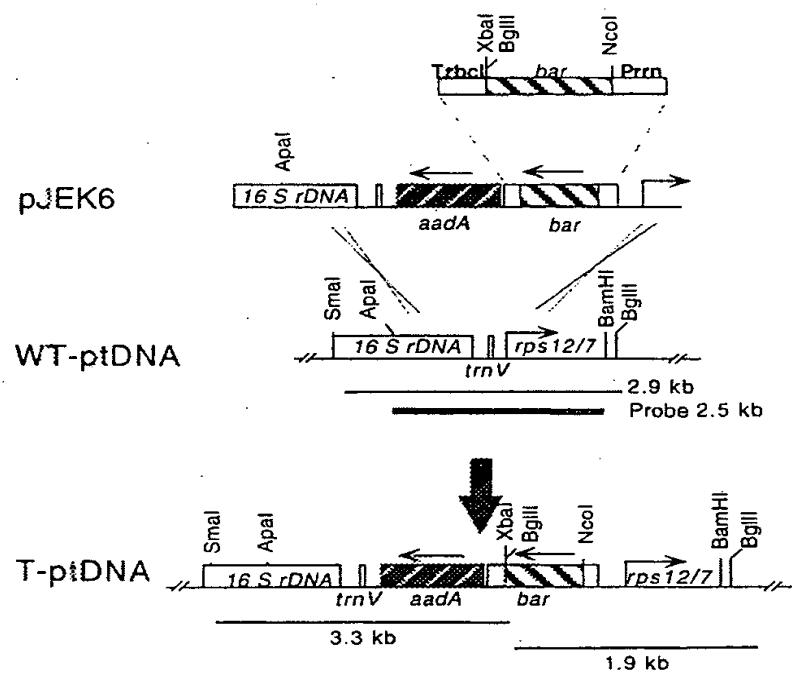


Figure 16A

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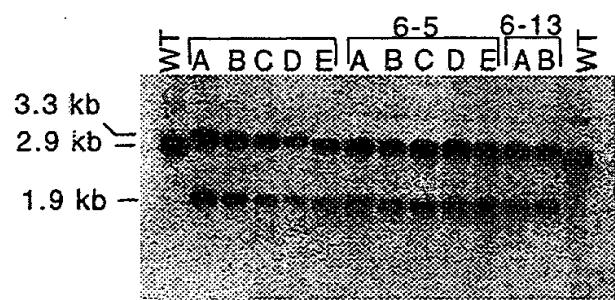


Figure 16B

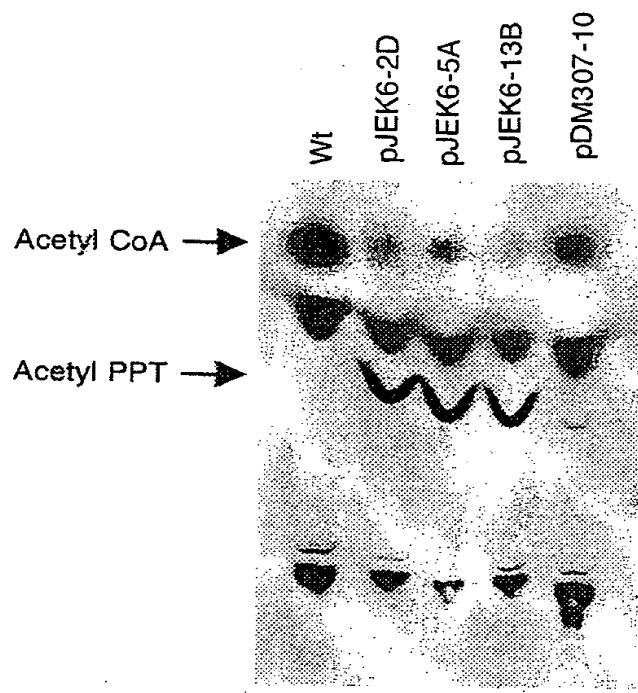


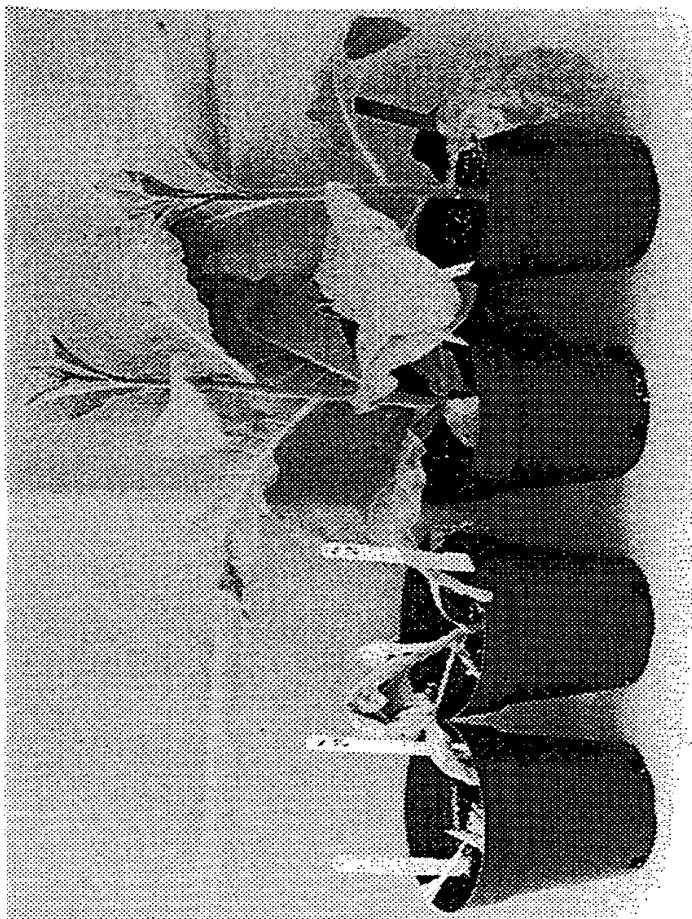
Figure 17

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Nt-6-2D Nt-6-5A Nt-wt Nt-wt

Figure 18A

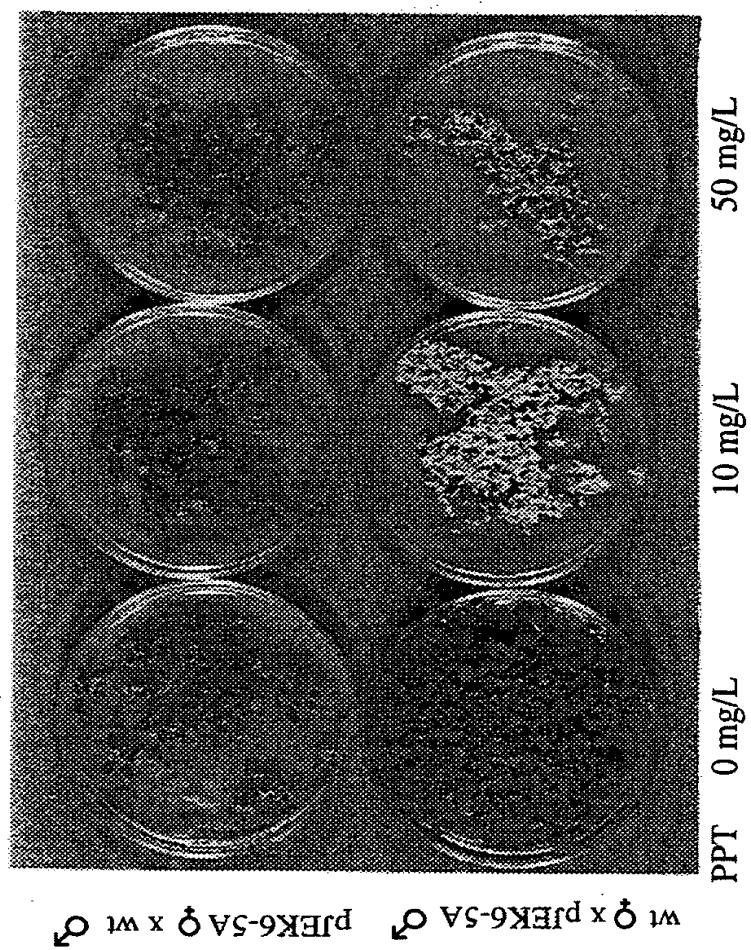


Figure 18B

NcoI

CCATGqcaccacaaaacagagAGCCCAGAACGACGCCGGCGACATCCGCCGTGCCACCG
-----+-----+-----+-----+-----+-----+-----+-----+ 60
GGTACcggtgggtttgttcTCGGGTCTGCTGCCGGCGCTGTAGGCAGCACGGTGGC
M A P Q T E S P E R R P A D I R R A T E

AGGC GGACATGCCGGCGGTCTGCACCACGTCAACCACATCGAGACAAGCACGGTCA
-----+-----+-----+-----+-----+-----+-----+-----+ 120
TCCGCCTGTACGGCCGCCAGACGTGGTAGCAGTTGGTATGTAGCTCTGTTCGTGCCAGT
A D M P A V C T I V N H Y I E T S T V N

ACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTCGTCCGTCTGCCGG
-----+-----+-----+-----+-----+-----+-----+-----+ 180
TGAAGGCATGGCTCGGCCTTGGCGTCCACCTGCCGTGCTGGAGCAGGCC
F R T E P Q E P Q E W T D D L V R L R E

AGCGCTATCCCTGGCTCGTCGCCGAGGTGGACGGCGAGGTGCGCCGGCATGCCCTACGCCG
-----+-----+-----+-----+-----+-----+-----+-----+ 240
TCGCGATAGGGACCGAGCAGCGCTCCACCTGCCGTCCAGCGCCGTAGCGGATGCC
R Y P W L V A E V D G E V A G I A Y A G

GCCCTGGAAGGCACGCAACGCCACGACTGGACGGCGAGTCGACCGTGTACGTCTCCC
-----+-----+-----+-----+-----+-----+-----+-----+ 300
CGGGGACCTTCCGTGCGTTGCGATGCTGACCTGCCGTAGCTGGCACATGCAGAGGG
P W K A R N A Y D W T A E S T V Y V S P

CCCGCCACCAGCGGACGGACTGGCTCCACGCTCTACACCCACCTGCTGAAGTCCCTGG
-----+-----+-----+-----+-----+-----+-----+-----+ 360
GGGCGGTGGTGCCTGCCCTGACCCGAGGTGCGAGATGTGGTGGACGACTTCAGGGACC
R H Q R T G L G S T L Y T H L L K S L E

AGGCACAGGGCTTCAAGAGCGTGGTCGCTGTCATCGGGCTGCCAACGACCCGAGCGTGC
-----+-----+-----+-----+-----+-----+-----+-----+ 420
TCCGTGTCCCAGAAGTTCTCGCACCGACAGTAGCCCGACGGTTGCTGGCTCGCACG
A Q G F K S V V A V I G L P N D P S V R

GCATGCACGAGGCCTCGGATATGCCCGCGCATGCTGCCGGCGCCGGCTTCAAGC
-----+-----+-----+-----+-----+-----+-----+-----+ 480
CGTACGTGCTCCCGAGCCATACGGGGGGCGCCGTACGACGCCCGCCGGCGAAGTCG
M H E A L G Y A P R G M L R A A G F K H

ACGGGAACCTGGCATGACGTGGTTCTGGCAGCTGGACTTCAGCCTGCCGGTACCGCCCC
-----+-----+-----+-----+-----+-----+-----+-----+ 540
TGCCTTGACCGTACTGCACCCAAAGACCGTGCACCTGAAGTCGGACGGCCATGGCGGG
G N W H D V G F W Q L D F S L P V P P R

BglII

GTCCGGTCCCTGCCCGTACCGAGATCTGATGAtcgaaattcctgcagccggggatccac
-----+-----+-----+-----+-----+-----+-----+-----+ 600
CAGGCCAGGACGGGCAGTGGCTCTAGACTACTagcttaaggacgtcgcccccctaggtg
P V L P V T E I *

XbaI

tagttctaga
-----+ 610
atcaagatct

Figure 19

NcoI NheI

CcATGGctAGCCCCAGAAaGAaGaCCGGCCGAtATTaGaCGTGctACaGAaGCtGAtATGC
 -----+-----+-----+-----+-----+-----+
 ggTACGcgATCGGGTCTtCTtCtGGCCGGCTaTAatCTgCACGATGtCTtCGaCTaTACG
 M A S P E R R P A D I R R A T E A D M P

CaGCaGTtTGtACaATtGTtAATCAtTAtATAaACAAGtACCGTaAACTTtcGaACtG
 -----+-----+-----+-----+-----+
 GtCGtCAaACaTGtTAaCAaTTaGTaATaTAtCTtTGTTCaTGgCAtTTGAAagCtTGaC
 A V C T I V N H Y I E T S T V N F R T E

AaCCtCAaGAACtCAaGAaTGGACtGAtGAttTaGTCCGtTaCGaGAGCGCTATCCtT
 -----+-----+-----+-----+-----+
 TtGGaGTtCTGGaGTtCTtACCTGtCACTaaAtCAGGCAaAtGtCTCGCgATAGGAA
 P Q E P Q E W T D D L V R L R E R Y P W

GGCTtGTaGCaGAaGTtGACGGaGAaGTaGCTGGgATtGCaTAtGCAGGGCCCgTGGAaA
 -----+-----+-----+-----+-----+
 CCGAaCAtCGtCTtCAaCTGCCtCTtCAtCGaCCtAAcGtATAcGCCCGGGcACCTTtC
 L V A E V D G E V A G I A Y A G P W K A

CAcGAAtGCATAtGAtTGGACgGCtGAaTCaACtGTgTACGtTCAccACGtCATCAaC
 -----+-----+-----+-----+-----+
 GTgCtTTaCGtATACTaACCTGcCGaCTtAGtTGaCACATGCAaAGtGGtGCaGTtG
 R N A Y D W T A E S T V Y V S P R H Q R

GgACaGGACTtGGtTCTtACttTaTAtACCCAtCTaCTGAAaTCTtTGGAGGCACAgGGtT
 -----+-----+-----+-----+-----+
 CcTGtCCTGAaCCaAGaTGaaAtATAtTGgGTaGAtGACTTtAGaaACCTCCGTGTcCCaA
 T G L G S T L Y T H L L K S L E A Q G F

TtAAGAGtGTgGTaGCTGTtATA GGatTGCCgAAAtGAtCCctcgGTaCGCATGCAcGAaG
 -----+-----+-----+-----+-----+
 AaTTCTCaACCAtCGACAAtCCtACGtCTaGGgacGtGCGTACGTgCTtC
 K S V V A V I G L P N D P S V R M H E A

CtCTCGGATATGctCCcaGaGGtATGtTGaGGGccGCAGGtTTCAAaCAtGGaAAtTGGC
 -----+-----+-----+-----+-----+
 GaGAGCCTATACGAaGGgtCtCCaTACaACtCCCGgCGtCCaAAGTTtGTaCCtTTaACCG
 L G Y A P R G M L R A A G F K H G N W H

ATGAtGTaGGTTTtTGGCAaCTtGAcTTCTttaCCaGTACCTCCtCGTCCGTTtTaC
 -----+-----+-----+-----+-----+
 TACTaCAtCCAAaACCGTtGAaCTgAAGagaaAtGGtCATGGAaGGaGCAGGgCAaaAtG
 D V G F W Q L D F S L P V P P R P V L P

BglII**XbaI**

CcGTtACtGAGATCTGATGAtctaga
 -----+-----+-----+
 GgCAaTGaCTCTAGACTACTagatct
 V T E I * *

Figure 20A

NcoI NheI

ccATGgctAGCCCAGAAaGAaGaCCGGCCGAtATtaGacGTGctACaGAaGCTGAtATGC
-----+-----+-----+-----+-----+
ggTACcgatCGGGTCTtCTtCtGCCGGCtaTAatCtGCACGATGtCTtCGaCTaTACG
M A S P E R R P A D I R R A T E A D M P

CaGCaGTtTGtACaATtGTtAAtCATtATAtaGAaACAAGtACaGTaAAAtTTtcGaACTG
-----+-----+-----+-----+-----+
GtCGtCAaACatGTtTAaCAaTTaGTaATtATtCTtTGTCaTGtCAtTTaAAagCt'GaC
A V C T I V N H Y I E T S T V N F R T E

AaCCtCAaGAACtCAaGAaTGGACtGAtGAtTaGTaCGtTaCGaGAaCGtTATCCtT
-----+-----+-----+-----+-----+
TtGGaGTtCTTGGaGTtCTtACCTGtCAaCTaaAtCAtGCAaAtGtCTtGCaATAGGaA
P Q E P Q E W T D D L V R L R E R Y P W

GGCTtGTaGCaGAaGTtGAcGGaGAaGTaGCTGGaATTGCaTAtGCTGGtCCgTGGAAaG
-----+-----+-----+-----+-----+
CCGAaCATCGtCTtCAaCTqCCtCTtCATCGaCCtTAaCGtATaCGaCCaGGcACCTTtC
L V A E V D G E V A G I A Y A G P W K A

CAcGaAAtGCaTAtGAtTGGACaGCTGAaTCaACtGTtTAtGTTtTCaCCaCGtCAtCAaC
-----+-----+-----+-----+-----+
GTgCtTTaCGtATaCTaACCTGtCGaCTtAGtTGaCAaATaCAaAGtGGtGCaGTaGTtG
R N A Y D W T A E S T V Y V S P R H Q R

GtACaGGACTtGGtCTtACttTaTAtACTCATCTtCTtAAaTCttTGGAAaGCACAAaGGtT
-----+-----+-----+-----+-----+
CaTGtCCTGAAccAAGaTGaaAtATaTGtAaGAaGAATTtAGaaACCTtCGTGTtCCAA
T G L G S T L Y T H L L K S L E A Q G F

TtAAaAGtGTaGTaGCTGTTAtGAtTGCCgAAtGAtCCctcaGTaCGCATGCAtGAaG
-----+-----+-----+-----+-----+
AaTTtTCaCAtCAtCGACAAtAtCCtaACGGcTTaCTaGGgagtCATGCGTACGTaCTtC
K S V V A V I G L P N D P S V R M H E A

CtCTtGGATATGctCCcaGaGGtATGtTGaGGGCaGCaGGtTTCAAACAtGGaAAAtTGGC
-----+-----+-----+-----+-----+
GaGAaCCTATAcGAaGGgtCTCCaTAcAACtCCCGtCGtCCaAAGTTtGTaCCtTTaACCG
L G Y A P R G M L R A A G F K H G N W H

ATGAtGTaGGTTTtTGGCAaCTtGAcTTCTtTaCCaGTACCTCCTCGTCCCGTttTAc
-----+-----+-----+-----+-----+
TACTaCAtCCAAAaACCGTtGAaCTgAAGagaaAtGGtCATGGaGGaGCAGGGCAaaAtG
D V G F W Q L D F S L P V P P R P V L P

BglII XbaI

CcGTtACTGAGATCTGATGAtctaqa
-----+-----+-----
GgCAaTGtCTCTAGACTACTagatct
V T E I * *

Figure 20B

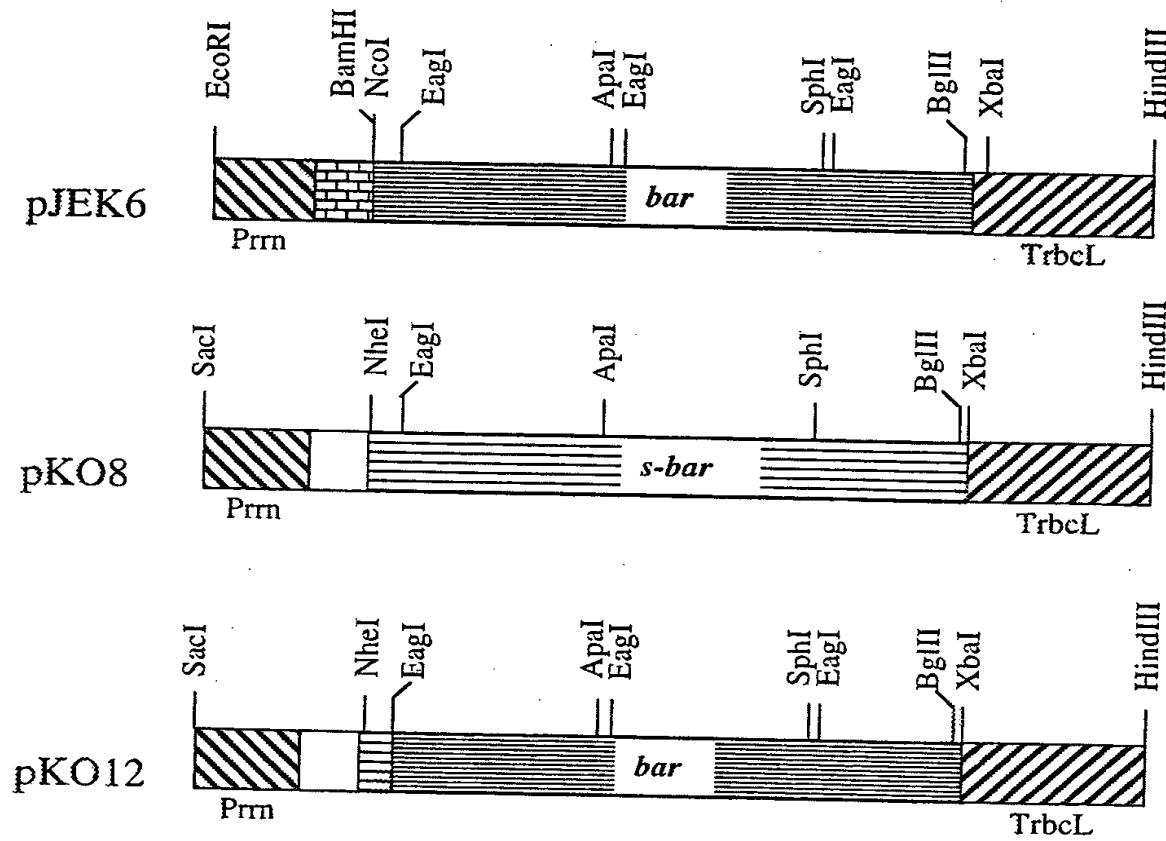


Figure 21

Bacterial Extracts



Figure 22A

09/762105

WO 00/07431

PCT/US99/17806

34/49

Plant Extracts



Figure 22B

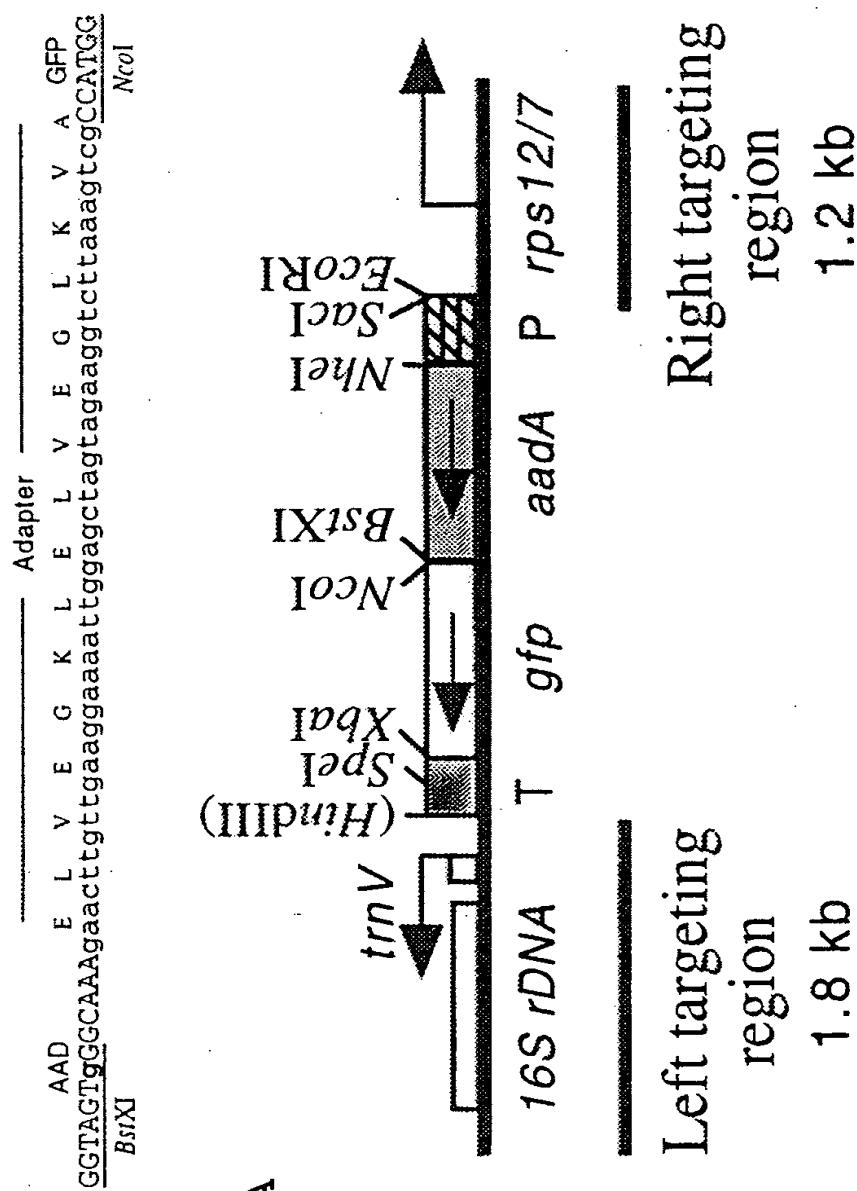


Figure 23B

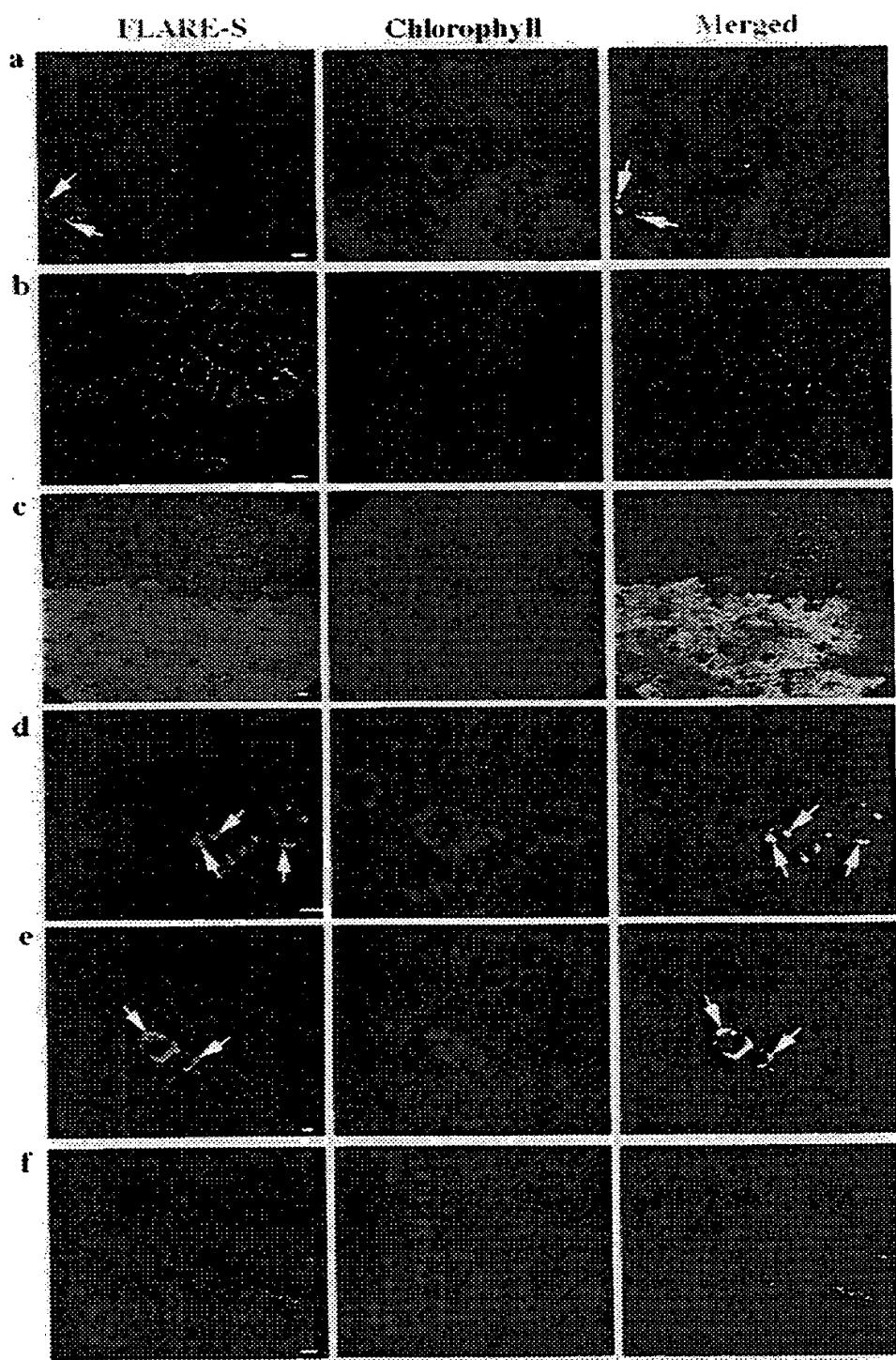


Figure 24

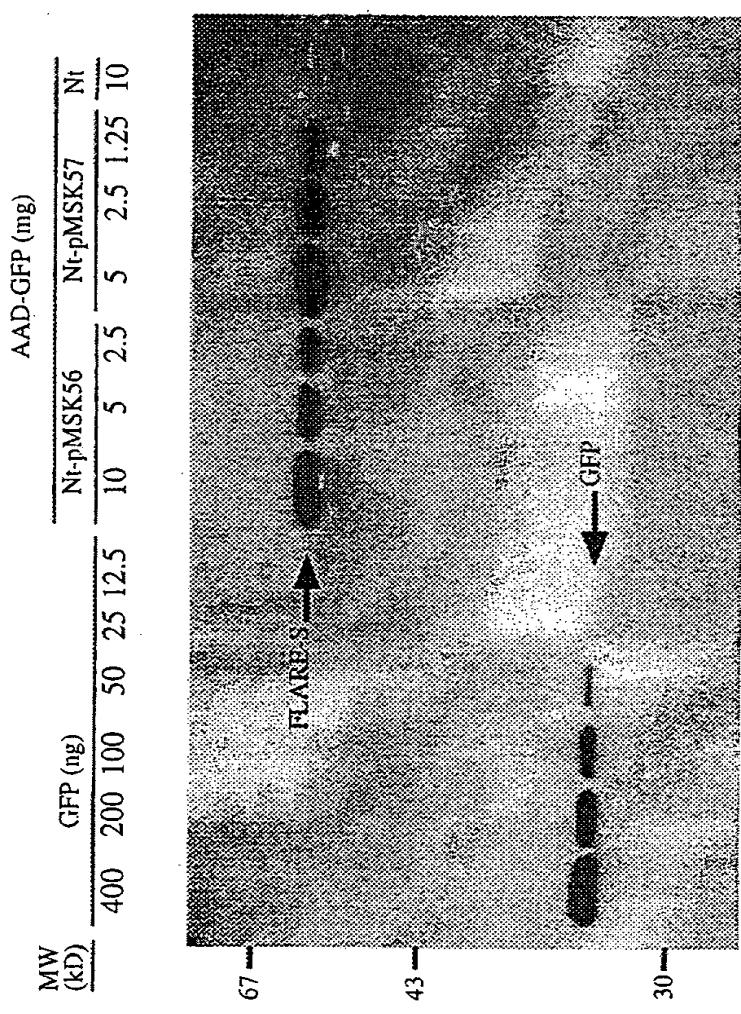
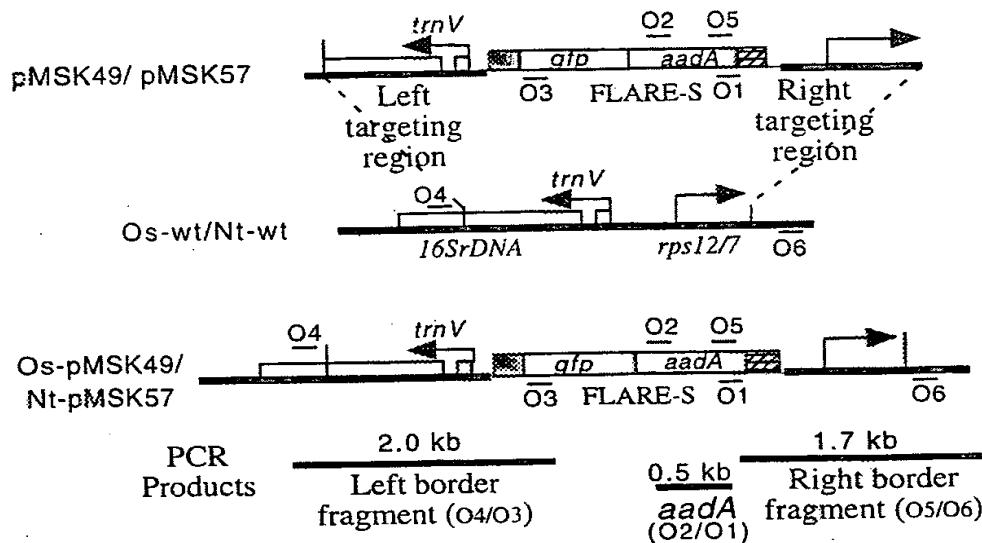
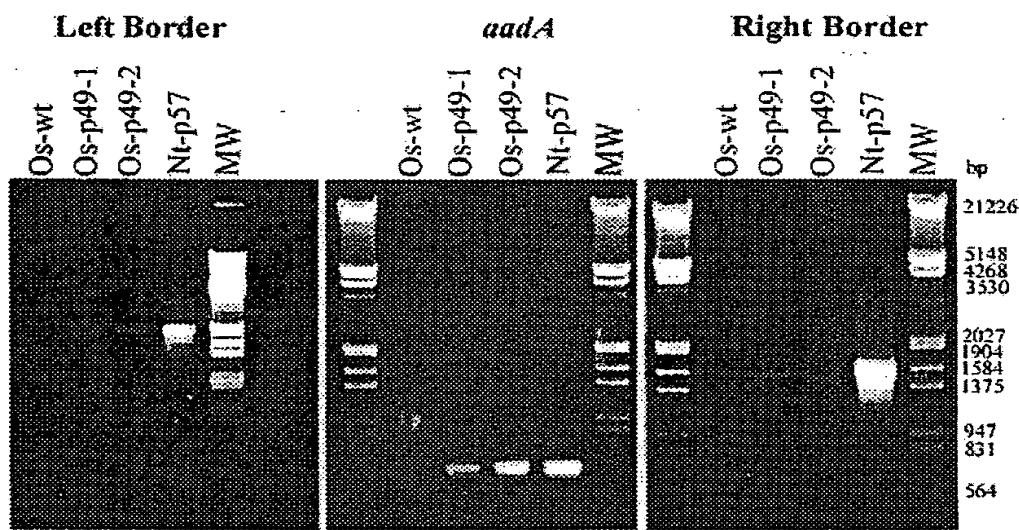


Figure 25

**Figure 26A****Figure 26B**

09/762105

PCT/US99/17806

WO 00/07431

39/49

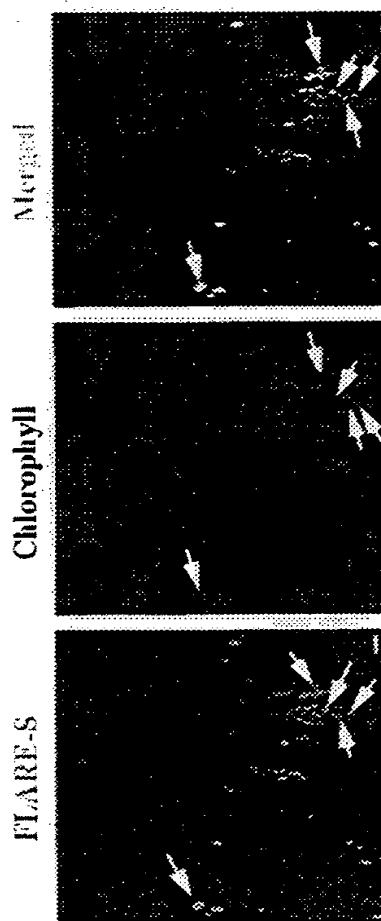


Figure 27

FLARE16-S.seq Length: 1574

NAT

1	ccATGgGGgc tagcGAAGCG	GTGATGCCG AAGTATCGAC	TCAACTATCA
51	GAGGTAGTTG GCGTCATCGA	GCGCCATCTC	GAACCGACGT TGCTGGCCGT
101	ACATTTGTAC GGCTCCGCAG	TGGATGGCGG	CCTGAAGCCA CACAGTGATA
151	TTGATTTGCT GGTTACGGTG	ACCGTAAGSC	TTGATGAAAC AACGCCGGCA
201	GCTTTGATCA ACGACCTTT	GGAAACTTCG	GCITCCCCTG GAGAGAGCGA
251	GATTC1CCGC GCTGTAGAAG	TCACCAATTGT	TGTGCACGAC GACATCATTC
301	CGTGGCGTTA TCCAGCTAAG	CGCGAACTGC	AATTGGAGA ATGGCAGCGC
351	AATGACATTG TTGCAGGTAT	CTTCGAGCCA	GCCACGATCG ACATTGATCT
401	GGCTATCTTG CTGACAAAAG	CAAGAGAACAA	TAGCGTTGCC TTGGTAGGTC
451	CAGCGGCCGA GGAACCTTT	GATCCGGTTC	CTGAACAGGA TCTATTTGAG
501	GCGCTAAATG AAACCTTAAAC	GCTATGGAAC	TCGCCCCCG ACTGGGCTGG
551	CGATGAGCGA AATGTAGTGC	TTACGTTGTC	CCGCATTGG TACAGCGCAG
601	TAACCGGCAA AATCGCCCG	AAGGATGTCG	CTGCGGACTG GGCATGGAG
651	CGCCTGCCGG CCCAGTATCA	GCCCCGTATA	CTTGAAGCTA GACAGGCTTA
701	TCTTGGACAA GAAGAAGATC	GCTTGGCCTC	GCGCGCAGAT CAGTTGGAAG
751	AATTGTCCTA CTACGTGAAA	GGCGAGATCA	CCAAGGTAGT gggcaaa_gaa
801	cttgttgaag gaaaatttgg	gctagttagaa	ggcttttaag tcgcctTGgc
851	TAGTAAAGGA GAAGAACTTT	TCACTGGAGT	TGICCCAAATT CTTGTTGAAT
901	TAGATGGTGA TGTAAATGGG	CACAAATTTT	CTGTCAGTGG AGAGGGTGAA
951	GGTGATGCAA CATA CGGAAA	ACTTACCCCTT	AAATTATTT GCACTACTGG
1001	AAAATACCT GTTCTTGTC	CAACACTTTG	CACTACTTTC TCTTATGGTG
1051	TTCAATGCTT TTCAAGATAC	CCAGATCATA	TGAAGCGGC CGACTTCTTC
1101	AAGAGCGCCA TGCCTGAGGG	ATACGTGCAG	GAGAGGACCA TCTCTTCAA
1151	GGACGACGGG AACTACAAGA	CACGTGCTGA	AGTCAAGTTT GAGGGAGACA
1201	CCCTCGTCAA CAGGATCGAG	CTTAAGGGAA	TCGATTCAA GGAGGACCGA
1251	AACATCCTCG GCCACAAGTT	GGAATACAAC	TACAACCTCC ACAACGTATA
1301	CATCACGGCA GACAAACAAA	AGAATGGAAT	CAAAGCTAAC TTCAAAATTA
1351	GACACAACAT TGAAGATGGA	ACCGTTCAAC	AGCAGACCA TTATCAACAA
1401	AATACTCCAA TTGGCGATGG	CCCTGTCCCTT	TTACCAAGACA ACCATTACCT
1451	GTCCACACAA TCTGCCCTT	CGAAAGATCC	CAACGAAAAG AGAGACCACA
1501	TGGTCCTTCT TGAGTTTGTA	ACAGCTGCTG	GGATTACACA TGGCATGGAT
1551	GAACTATACA AATAAGgttc	tada	

XbaI

addA

gfp

Figure 28

FLARE16-S1.seq Length: 1953

SacI

1	gagctcgCTC	CCCCGCCGTC	GTTCAATGAG	AATGGATAAG	AGGCTCGTGG
51	GATTGACGTG	AGGGGGCAGG	GATGGCTATA	TTTCTGGGAG	TCGAGTAGAC
101	CTTGTGTG	TGAaAATTCT	TAATTCACTGA	GTTGTAGGGA	GGGATTATG
151	TCACCACAAA	CAGAGACTAA	AGCAAGTGT	GGATTCAAAG	ctagc ^{TAAGC}
201	GGTGATCGCC	GAAGTATCGA	CTCAACTATC	AGAGGTAGTT	GGCGTCATCG
251	AGCGCCATCT	CGAACCGACG	TTGCTGGCCG	TACATTTGTA	CGGCTCCGCA
301	GTGGATGGCG	GCCTGAAGCC	ACACAGTGT	ATTGATTTCG	TGGTTACGGT
351	GACCGTAAGG	CTTGATGAAA	CAACGCCGCG	AGCTTTGATC	AACGACCTTT
401	TGGAAACTTC	GGCTTCCCT	GGAGAGAGCG	AGATTCTCCG	CGCTGTAGAA
451	GTCACCATTG	TTGTGCACGA	CGACATCATT	CCGTGGCGTT	ATCCAGCTAA
501	GGCGGAAC TG	CAATTGGAG	AATGGCAGCG	CAATGACATT	CTTGCAGGTA
551	TCTTCGAGCC	AGCCACGATC	GACATTGATC	TGGCTATCTT	GCTGACAAAAA
601	GCAAGAGAAC	ATAGCGTTGC	CTTGGTAGGT	CCAGCGGCCG	AGGAACCTTT
651	TGATCCGGTT	CTTGAACAGG	ATCTATTGTA	GGCGCTAAAT	GAAACCTTAA
701	CGCTATGGAA	CTCGCCGCC	GACTGGGCTG	GGCATGAGCG	AAATGTAGTG
751	CTTACGTTGT	CCCGCATTG	GTACAGCGCA	GTAACCGGCA	AAATCGCGCC
801	GAAGGATGTC	GCTGCCGACT	GGGCAATGGA	GCGCTGCCG	GCCCAGTATC
851	AGCCCGTCAT	ACTTGAAGCT	AGA CAGGCTT	ATCTTGGACA	AGAAGAAGAT
901	CGCTTGGCCT	CGCGCCGAGA	TCAGTGGAA	GAATTGTCC	ACTACGTGAA
951	AGGGCAGATC	ACCAAGGTAG	T GGCAAA ga	acttggtaa	ggaac ttgg
1001	agctagtaga	aggctttaaa	gtcgccATGG	CTAGTAAAGG	AGAAGAACTT
1051	TTCACTGGAG	TTGTCCCAAT	TCTTGTGAA	TTAGATGGT	ATGTTAATGG
1101	GCACAAATT	TCTGTCAGTG	GAGAGGGTGA	AGGTGATGCA	ACATACGGAA
1151	AACTTACCC	TAATTATT	TGCACTACTG	GAAAAC TACC	TGTTCCCTGG
1201	CCAACACTTG	TCACTACTT	CTCTTATGGT	GTTCAATGCT	TTTCAAGATA
1251	CCCAGATCAT	ATGAAGCGGC	ACGACTTCTT	CAAGAGCGCC	ATGCCCTGAGG
1301	GATACGTGCA	GGAGAGGACC	ATCTCTTCA	AGGACGACGG	GAAC TACAAG
1351	ACACGTGCTG	AAGTCAGTT	TGAGGGAGAC	ACCTCGTCA	ACAGGATCGA
1401	GCTTAAGGGA	ATCGATTCA	AGGAGGACGG	AAACATCCTC	GGCCACAAAGT
1451	TGGAATACAA	CTACAACCTC	CACAACTAT	ACATCACGGC	AGACAAACAA
1501	AAAGAATGGAA	TCAAAGCTAA	CTTCAAAATT	AGACACAACA	TTGAAGATGG
1551	AAAGCGTTCAA	CTAGCAGAC	ATTATCAACA	AAATACTCCA	ATTGGCGATG
1601	GCCCTGTCT	TTTACCAAGAC	AACCATTAC	TGTCCACACA	ATCTGCCCTT
1651	TCGAAAGATC	CCAACGAAA	GAGAGACCAC	ATGGTCCTTC	TTGAGTTTG
1701	AAACAGCTGCT	GGGATTACAC	ATGGCATGGA	TGAACATATAC	AAATAAGGCT
1751	ctagagc GAT	CCTGCCCTAG	TCTATAGGAG	GT TTT GA AAA	GAAAGGAGCA
1801	ATAATCATTT	TCTTGTCTA	TCAAGAGGGT	GCTATTGCTC	CTTTCTTTT
1851	TTCTTTTAT	TTATTACTA	GTATTACT	TACATAGACT	TTTTGTITTA
1901	CATTATAGAA	AAAGAAGGAG	AGGTTATTTT	CTTGCATTTA	TTCATGaaag
1951	c tt				Hind III

*Lap823**ada**gfp**TpsB*

Figure 29

FLARE16-S2.seq Length: 1985

SacI

1	gagctcGCTC	CCCCGGCCGTC	GTTCAATGAG	AATGGATAAG	AGGCTCGTGG
51	GATTGACGTG	AGGGGGCAGG	GATGGCTATA	TTTCTGGAG	AATTAACCGA
101	TCGACGTGCa	AGCGGACATT	TATTTAAAT	TCGATAATT	TTGCAAAAAC
151	ATTCGACAT	ATTTATTAT	TTTATTATTA	TGAGAATCAA	TCCTACTACT
201	TCGGITCTG	GGGGTTCCAC	GgctagcGAA	GCGGTGATCG	CCGAAGTATC
251	GAECTCAACTA	TCAGAGGTAG	TTGGCGTCAT	CGAGGCCAT	CTCGAACCGA
301	CGTTGCTGGC	CGTACATTG	TACGGCTCCG	CAGTGGATGG	CGGCCTGAAG
351	CCACACAGTG	ATATTGATT	GCTGGTACG	GTGACCGTAA	GGCTTGATGA
401	AAACAACCGG	CGAGCTTGA	TCAACGACCT	TTTGGAAACT	TCGGCTTCCC
451	CTGGAGAGAG	CGAGATTCTC	CGCGCTGTAG	AAGTCACCAT	TGGTGTGCAC
501	GACGACATCA	TTCCGTGGCG	TTATCCAGCT	AAGCGCGAAC	TGCAATTGG
551	AGAATGGCAG	CGCAATGACA	TTCTTGCAGG	TATCTTCGAG	CCAGCCACGA
601	TCGACATTGA	TCTGGCTATC	TTGCTGACAA	AAGCAAGAGA	ACATAGCGTT
651	GCCTTGGTAG	GTCAGCGGC	GGAGGAACCTC	TTTGATCCGG	TTCTGAACA
701	GGATCTATT	GAGGCCTAA	ATGAAACCTT	AACGCTATGG	AACTCGCCGC
751	CCGACTGGGC	TGGCGATGAG	CGAAATGTAG	TGCTTACGTT	GTCCCGCAT
801	TGGTACAGCG	CAGTAACCAGG	AAAATCGCG	CCGAAGGATG	TCGCTGCCGA
851	CTGGGCAATG	GAGCGCCTGC	CGGCCAGTA	TCAGCCCGTC	ATACTTGAAG
901	CTAGACAGGC	TTATCTTGG	CAAGAAGAAG	ATCGCTTGGC	CTCGCGCGCA
951	GATCAGTTGG	AAAGAATTGT	CCACTACGTG	AAAGGGCAGA	TCACCAAGGT
1001	AGtggggCAA	aaacttgg	aaggaaaaatt	ggagctagta	gaaggcttta
1051	aagtgcgcAT	GgcTAGTAA	CGAGAAGAAC	TTTCACTGG	AGTTGTCCCA
1101	ATTCTTGTG	AAATTAGATGG	TGATGTTAAT	GGGCACAAAT	TTTCTGTCA
1151	TGGAGAGGGT	GAAGGTGATG	CAACATACGG	AAAACCTTAC	CTTAAATT
1201	TTTGCACTAC	TGGAAAAC	CCTGTTCC	GGCCAACACT	TGTCACTACT
1251	TTCTCTTATG	GTGTTCAATG	CTTTCAAGA	TACCCAGATC	ATATGAAGCG
1301	GCACGACTTC	TTCAAGAGCG	CCATGCCTGA	GGGATACGTG	CAGGAGAGGA
1351	CCATCTCTT	CAAGGACGAC	GGGAACATACA	AGACACGTGC	TGAAGTCAAG
1401	TTTGAGGGAG	ACACCCCTCGT	CAACAGGATC	GAGCTTAAGG	GAATCGATT
1451	CAAGGAGGAC	GGAAACATCC	TCGGCACAA	GTTGGAATAC	AACTACAACT
1501	CCCACAAACGT	ATACATCAGC	GCAGACAAAC	AAAAGAATGG	AATCAAAGCT
1551	AACTTCAAA	TTAGACACAA	CATTGAAGAT	GGAAGCGTTC	AACTAGCAGA
1601	CCATTATCAA	CAAAATACTC	CAATGGCGA	TGGCCCTGTC	CTTTTACCA
1651	ACAACCATT	CCTGTCCACA	CAATCTGCC	TTTCGAAGA	TCCCAACGAA
1701	AAGAGAGACC	ACATGGTCCT	TCTTGAGTT	CTAACAGCTG	CTGGGATTAC
1751	ACATGGCATG	GATGAACAT	ACAAATAAG	ctctagagc	ATCCTGGCC
1801	AGTCTATAGG	AGGGTTTGAA	AAGAAAGGAG	CAATAATCAT	TTTCTTGTTC
1851	TATCAAGAGG	GTGCTATTGC	TCCTTCTTT	TTTCTTTT	ATTATTTAC
1901	TAGTATT	TTAACATAGA	CTTTTTGTT	TACATTATAG	AAAAAGAAGG
1951	AGAGGTTATT	TTCTTGATT	TATTCATGaa	agctt	

*HindIII**LtrB1* DB*adA**gfp**ThsA*

Figure 30

FLARE11-S.seq Length: 1595

NcoI *C-Myc*

1	ccatggggc tagcgaacaa aaactcattt ctgaagaaga cttgccttagc
51	GAAGCGGTGA TCGCCGAAGT ATCGACTCAA CTATCAGAGG TAGTTGGCGT
101	CATCGAGCGC CATCTCGAAC CGACGTTGCT GGCCGTACAT TTGTACGGCT
151	CCGCAGTGGT TGGCGGCCCTG AAGCCACACA GTGATATTGA TTTGCTGGTT
201	ACGGTGACCG TAAGGCTTGA TGAAACAACG CGGCGAGCTT TGATCAACGA
251	CCTTTGGAA ACTTCGGCTT CCCCTGGAGA GAGCGAGATT CTCCGCGCTG
301	TAGAAGTCAC CATTGTTGTC CACGACGACA TCATTCCGTG GCGTTATCCA
351	GCTAAGCGCG AACTGCAATT TGGAGAATGG CAGCGCAATG ACATTCTTGC
401	AGGTATCTTC GAGCCAGCCA CGATCGACAT TGATCTGGCT ATCTTGCTGA
451	CAAAAGCAAG AGAACATAGC GTTGCCTTGG TAGGTCCAGC GGCAGGAGGA
501	CTCTTGATC CGGTTCCCTGA ACAGGATCTA TTTGAGGCAGC TAAATGAAAC
551	CTTAACGCTA TGGAACTCGC CGCCCGACTG GGCTGGCGAT GAGCGAAATG
601	TAGTGCTTAC GTTGTCCCCG ATTTGGTACA GCGCAGTAAC CGGCAAATC
651	GCGCCGAAGG ATGTCGCTGC CGACTGGGCA ATGGAGCGCC TGCCGGCCCA
701	GTATCAGCCC GTCATACTTG AAGCTAGACA GGCTTATCTT GGACAAGAAG
751	AAGATCGCTT GGCCCTCGCGC GCAGATCAGT TGGAGAAATT TGTCCACTAC
801	GTGAAAGGCG AGATCACCAA GGTAGTGGC AAAaacttg cagttgaagg
851	aaaatttggag ctgcgcATGG ctAGTAAAGG AGAAGAACTT TTCACTGGAG
901	TTGTCCTAAT TCTTGTGAA TTAGATGGTG ATGTTAATGG GCACAAATT
951	TCTGTCAGTG GAGGAGGTGA AGGTGATGCA ACATACGGAA AACTTACCC
1001	AAAATTATT TGCACTACTG GAAAACCTACC TGTTCC-TGG CCAACACTTG
1051	TCACTACTTT CTCTTATGGT GTTCAATGCT TTTCAAGATA CCCAGATCAT
1101	ATGAAGCGGC ACCACTTCTT CAAGAGCGCC ATGCCTGAGG GATACTGCA
1151	GGAGAGGACC ATCTCTTCA AGGACGACGG GAACTACAAG ACACGTGCTG
1201	AAGTCAGTT TGAGGGAGAC ACCCTCGTCA ACAGGATCGA GCTTAAGGGAA
1251	ATCGATTCA AGGAGGACGG AAACATCTC GGCCACAAGT TGAATACAA
1301	CTACAACCTCC CACAACGTAT ACATCACGGC AGACAAACAA AAGAATGGAA
1351	TCAAAGCTAA CTTCAAAATT AGACACAAAC- TTGAAGATGG AAGCGTTCAA
1401	CTAGCAGACC ATTATCAACA AAATACTCCA ATTGGCGATG GCCCTGTCCT
1451	TTTACCAAGAC AACCAATTACG TGTCCACACCA ATCTGCCCTT TCGAAAGATC
1501	CCAACGAAAA GAGAGACCAAC ATGGTCCTTC TTGAGTTGT AACAGCTGCT
1551	GGGATTACAC ATGGCATGGA TGAACATAC AAATAAGgtc ctaga

XbaI

addA

Zfp

Figure 31

FLARE11-S3.seq Length: 1961

SacI

1	gagctcgctc	CCCCGCCGTC	GTTCAATGAG	AATGGATAAG	AGGCTCGTGG
51	GATTGACGTG	AGGGGGCAGG	GATGGCTATA	TTTCTGGAG	GGAGACCA
101	ACGGTTTCCC	actAGAAATA	ATTTGTTA	ACTTTAAGAA	GGAGATATA
151	ATATGGCaAG	CATGACTGGT	GGACAG	gcta	gcgaacaaaa
201	gaagaagact	tgccttagcfa	AGCGGTGATC	GCCGAAGTAT	CGACTCAACT
251	ATCAGAGGT	GTGGCGTCA	TCGAGCGCCA	TCTCGAACCG	ACGTTGCTGG
301	CCGTACATT	GTACGGCTCC	GCAGTGGATG	GCGGCCTGAA	GCCACACAGT
351	GATATTGATT	TGCTGGTTAC	GGTGACCGTA	AGGCTTGATG	AAACAACGCG
401	GCGAGCTTG	ATCAACGACC	TTTGGAAAC	TTCGGCTTCC	CCTGGAGAGA
451	GCGAGATTCT	CCCGCGCTGTA	GAAGTCACCA	TTGTTGTGCA	CGACGACATC
501	ATTCCGTGGC	GTATTCAGC	TAAGCGCAA	CTGCAATTG	GAGAATGGCA
551	GCGCAATGAC	ATTCTTGCAG	GTATCTTCGA	GCCAGCCACG	ATCGACATTG
601	ATCTGGCTAT	CTTGCTGACA	AAAGCAAGAG	AACATAGCGT	TGCCTTGGTA
651	GGTCCAGCGG	CGGAGGAAC	CTTTGATCCG	GTTCTGAAAC	AGGATCTATT
701	TGAGGGCGTA	AATGAAACCT	TAACGCTATG	GAACTCGCCG	CCCGACTGGG
751	CTGGCGATGA	GCGAAATGTA	GTGCTTACGT	TGTCCCGCAT	TTGGTACAGC
801	GCAGTAACCG	GCAAAATCGC	GCGGAAGGAT	GTCGCTGCCG	ACTGGGCAAT
851	GGAGCGCCTG	CCGGCCCAAGT	ATCAGCGCGT	CATACTGAA	GCTAGACAGG
901	CTTATCTTGG	ACAAGAAGAA	GATCGCTTGG	CCTCGCGCGC	AGATCAGTTG
951	GAAGAATTG	TCCACTACGT	GAAAGCGAG	ATCACCAAGG	TAGTggGCAA
1001	gaacttgc	gttggaggaa	aattggaggt	cgccATGgc	AGTAAAGGAG
1051	AAGAACCTTT	CACTGGAGTT	GTCCCAATT	TTGTTGAATT	AGATGGTGAT
1101	GTAAATGGC	ACAAAATTT	TGTCAGTGG	GAGGGTGAAG	GTGATGCAAC
1151	ATACGGAAAA	CTTACCCCTTA	AATTATTTG	CACTACTGGA	AAACTACCTG
1201	TTCCCTGGCC	AACACTTGT	ACTACTTCT	CTTATGGTGT	-TCAATGCTTT
1251	TCAAGATACC	CAGATCATAT	GAAGCGGCAC	GACTTCTCA	AGAGCGCCAT
1301	GCCTGAGGG	TACGTGCGAG	AGAGGACCAT	CTCTTCAAG	GACGACGGGA
1351	ACTACAAGAC	ACGTGCTGAA	GTCAAGTTG	AGGGAGACAC	CCTCGTCAAC
1401	AGGATCGAGC	TTAAGGGAAT	CGATTCAAG	GAGGACGGAA	ACATCCTCGG
1451	CCACAAGTTG	GAATACAAC	ACAACCTCCA	CAACGTATAC	ATCACGGCAG
1501	ACAAACAAAA	GAATGGAATC	AAAGCTAAT	TCAAAATTAG	ACACAAACATT
1551	GAAGATGGAA	GGCTTCAACT	AGCAGACCAT	TATCAACAAA	ATACTCCAAT
1601	TGGCGATGGC	CCTGTCTTT	TACCAACAA	CCATTACCTG	TCCACACAA
1651	CTGCCCTTTC	GAAAGATCCC	AACGAAAAGA	GAGACCAT	GGTCCTTCTT
1701	GAGTTTGTAA	CAGCTGCTGG	GATTACACAT	GGCATGGATG	AACTATACAA
1751	ATAAGgtct	agagcGATCC	TGGCCTAGTC	TATAGGAGGT	TTTGAAGAGA
1801	AAAGGAGCAAT	AATCAATTTC	TTGTTCTATC	AAGAGGGTGC	TATTGCTCCT
1851	TTCTTTTTT	CTTTTATT	ATTACTAGT	ATTTTACTTA	CATAGACTTT
1901	TTTGTGTTACA	TTATAGAAAA	AGAAGGAGAG	GTTATTTCT	TGCATTATT
1951	CATGaaagct	t			

Himat

Figure 32

pMSK35.seq Length: 4671

Figure 33A

• 122488

GGGAAACGGAT TCACCGCCGT ATGGCTGACC GGCAGATTACT AGCGATTCT
 1 GCTTCATGCA GGCAGITTCG AGCCTGCAAT CCGAACTGAG GACGGGTTT
 51 TGGAGTTAGC TCACCCCTCGC GAGATCGCGA CCCTTTGTCC CGCCCCATTGT
 101 AGCACGTGTG TCGCCCAGGG CATAAGGGGC ATGATGACTT GCCCTCATCC
 151 TCTCCTTCCT CGGGCTTAAC ACCGGCGGTC TGTTCAAGGGT TCCAAACTCA
 201 TAGTGGCAAC TAAACACGAG GGTTGGCGTC GTTGCAGAC TTAACCCAAC
 251 ACCTTACGGC ACGAGCTGAC GACAGCCATG CACCACCTGT GTCCCGCGTTC
 301 CCGAGGGCAC CCCTCTCTT CAAGAGGATT CGCGGCCATGT CAAGCCCTGG
 351 TAAGGTTCTT CGCTTGCAT CGAATTAAAC CACATGCTCC ACCGCTTGTG
 401 CGGGCCCCCG TCAATTCCCT TGAGTTTCAT TCTTGCAGAC GTACTCCCCA
 451 GGCGGGATAC TTAACCGGT AGCTACAGCA CTGCACGGGT CGAGTCGGCAC
 501 AGCACCTAGT ATCCATCGTT TACGGCTAGG ACTACTGGGG TCTCTAATCC
 551 CATTGCTCC CCTAGCTTC GTCTCTCAGT GTCAGTGTG GCCCAGCAGA
 601 GTGCTTTCGC CGTTGGTGT CTTCCTCGATC TCAATGCATT TCACCGCTCC
 651 ACCGGAAATT CCCTCTGCCCT ACACCGTACT CCAGCTTGGT AGTTTCCACC
 701 GCCTGTCCAG GGTTGAGCCC TGGGATTGAA CGCGGGACTT GAAAAGCCAC
 751 CTACAGACGC TTACGCCCCA ATCATTCCGG ATAACGCTTG CATCCTCTGT
 801 CTTACCGCGG CTGCTGGCAC AGAGTTAGCC GATGCTTATT CCTCAGATAC
 851 CGTCATTGTT TCTTCTCCGA GAAAAGAAGT TGACGACCCG TGGGCCTTCC
 901 ACCTCCACGC GGCATTGCTC CGTCAGGCTT TCGCCCATG CGGAAAATTG
 951 CCCACTGCTG CCTCCCGTAG GAGTCTGGC CGTGTCTCAG TCCCAGTGTG
 1001 GCTGATCATC CTCTCGGACC AGCTACTGAT CATGCCCTTG GTAAGCTATT
 1051 GCCTCACCAA CTAGCTAAC AGACCGCGAGC CCCTCCTTGG GCGGATTCT
 1101 CCTTTGCTC CTAGCCTAC GGGGTATTAG CAACCGTTTC CAGTTGTG
 1151 TCCCCCTCCA AGGGCACTT CTACGCGTT ACTCACCGT TCGCCACTGG
 1201 AACACCACT TCCCCTTCGA CTGCGATGTG TTAAGCATGC CGCCAGCGTT
 1251 CATCCTGAGC CAGGATCGAA CTCTCCATGA GATTCTAGT TGCAATTACTT
 1301 ATAGCTTCCT TATTGTTAGA CAAAGCGGAT TCGGAATTGT CTTTCCCTTCC
 1351 AAGGATAACT TGATCCATG CGCTTCAGAT TATTAGCCTG GAGTTCGCCA
 1401 CCAGCAGTAT AGCCAACCC ACCCTATCAC GTCAATCCCA CAAGCCTCTT
 1451 ATCCATTCCC GTTCGATCGT GGCGGGGGAA GTAAAGTCAAA ATAGAAAAAA
 1501 CTCACATTGG GTTAGGGAT AATCAGGCTC GAACTGATGA CTTCACCCAC
 1551 GTCAAGGTGA CACTCTACCG CTGAGTTATA TCCCTCCCT GTCCTCTCGA
 1601 GAAAGAGAAT TACCGAATCC TAAGGCAAAG GGGCGAGAAA CTCAAGGCCA
 1651 CCCTTCCTCC GGGCTTTCTT TCCACACTAT TATGGATAGT CAAATAATGG
 1701 GAAAAATTGG ATTCAATTGT CAACCGGTCC TATCGAAAAT AGGATTGACT
 1751 ATGGATTGCA GCCATAGCAC ATGGTTTCAT AAAATCTGTA CGATTTTCCC
 1801 GATCTAAATC GAGCAGGTTT CCATGAAGA gatcgacgg atcgataaagc
 1851 ttgcattgtt gcaggtaaaa TATAAGCTCTT CTTTCTTATT TCAATGATAT
 1901 TATTATTTCA AAGATAAGAG ATATTCAAAG ATAAGAGATA AGAAGAAGTC
 1951 AAAATTGAT TTTTTTTTG GAAAAAAAAA ATCAAAAAGA TATAGTAACA
 2001 TTAGCAAGAA GAGAAACAAG TTCTATTCA CAATTAAAC AAATACAAAA
 2051 TCAAAATAGA ATACTCAATC ATGAATAAAAT GCAAGAAAAT AACCTCTCCT
 2101 TCTTTTCTA TAATGTAAC AAAAAAGTCT ATGTAAGTAA AATACTAGTA
 2151 AATAAATAAA AAGAAAAAAA GAAAGGAGCA ATAGCACCCCT CTTGATAGAA
 2201 CAAGAAAATG ATTATTGCTC CTTTCTTTTC AAAACCTCCT ATAGACTAGG
 2251 CCAGGATGATGCTC tcttagttaga CATTATTTGC CGACTACCTT GGTGATCTCG
 2301 CCTTTCACTG AGTGGACAAA TTCTTCCAAC TGATCTGCGC GCGAGGCCAA
 2351 GCGATCTCT TCTTGTCCAA GATAAGCCTG TCTAGCTTCA AGTATGACGG
 2401 GCTGATACTG GGCGGGCAGG CGCTCCATTG CCCAGTCGGC AGCGACATCC
 2451 TTCGGCGCGA TTTTGGCGGT TACTGCGCTG TACCAAATGC GGGACAAACGT
 2501 AAGCACTACA TTTGCTCAT CGCCAGCCCA GTCGGGCGGC GAGTTCCATA
 2551 GCGTTAAAGT TTCAATTAGC GCCTCAAATA GATCCTGTTC AGGAACCGGA
 2601 TCAAAGAGTT CCTCCGCCGC TGGACCTACC AAGGCAACGC TATGTTCTCT
 2651 TGCTTTGTC AGCAAGATAG CCAGATCAAT GTCGATCGTG GCTGGCTCGA
Rice left targeting sequence
idat

09/762105
PCT/US99/17806

WO 00/07431

46/49

pMSK35.seq Length: 4671

2751 AGATAACCTGC AAGAATGTCA TTGCGCTGCC ATTCTCCAAA TTGCAGTTCG
2801 CGCTTAGCTG GATAACGCCA CGGAATGATG TCGTCGTGCA CAACAATGGT
2851 GACTTCTACA GCGCGGAGAA TCTCGCTCTC TCCAGGGGAA GCCGAAGTTT
2901 CCAAAAGGTC GTTGATCAA GCTCGCCGCG TTGTTTCATC AAGCCTTACG
2951 GTCACCGTAA CCAGCAAATC AATATCACTG TGTGGCTTCA GGCGGCCATC
3001 CACTGCGGAG CCGTACAAAT GTACGCCAG CAACGTCGGT TCGAGATGGC
3051 GCTCGATGAC GCCAACTACC TCTGATAGTT GAGTCGATAC TTCCGGCGATC
3101 ACCGCTTCCC TCATGGATCC CTCCCTACAA CTGTATCCAa GCGCTTCgTA
3151 TTCGCCCGGA GTTCGCTCCC AGAAATATAG CCATCCCTGC CCCCTCACGT
3201 CAATCCACG AGCCTCTTAT CCATTCTCAT TGAACGACGG CGGGGGAGC
3251 ttgggtaccc agctcgaatt cctgcagccc gatcttACCA TTTCCGAAGG
3301 AACTGGGCT ACATTTCTT TCAATTCTCA TTCAAGAGTT TCTTATCTGT
3351 TTCCACGCC CTTTTTGAGA CCTCGAAACA TGAAATGGAC AAATTCCITC
3401 TCTTAGGAAC ACATACAAGA AAAAGGATAA TGGTAGCCCT CCCATTAACT
3451 ACTTCATTTC ATTTATGAAT TTCATAGTAA TAGAAATCCA TGTCTTACCG
3501 AGACAGAAATT TCGAACITGC TATCCTCTTG CCTAATAGGC AAAGATTGAC
3551 CTCTGTAGAA AGAATGATTG ATTCGGATCG ATATGAGGAC CCAACTACGT
3601 TGCATTGCAAG AATCCATGTT CCATATTGAGA AGAGGGTTGA CCTCTGTGCT
3651 TCTCTCATGG TACAATCTC TTCCGTGTA GCCCCCCTTTC TCCTCGGTCC
3701 ACAGAGAAAA ATGGAGGAC TGTTGGGAC AGTTCATCAC GGAAGAAAGA
3751 ACTCACAGAG CCGGGATCGC TAACTAATAG AATAGTACTA CTAACATAATA
3801 CTAATATATA GAAATAGATA TctagctagA AATAGAAACA ACTAATATAT
3851 AGATAATCGA AATTGAAAAG AACTGTCTT TCTGTATACT TTCCCCGTTC
3901 TATTGCTTACCG GCGGGTCTTA TGCAATCGAT CGGATCATAT AGATATCCCT
3951 TCAACACAAAC ATAGGTCTAC GAAAGGATCT CGGACGACTC ACCAAAGCAO
4001 GAAAGCCAGT TAGAAAATGG ATTCCCTATT TGAAGAGTGCC TAACCGCATG
4051 GATAAGCTCA CATTAAACCCG TCAATTGTTG ATCCAATTGAG GGATTTTCT
4101 TGGGAAGTTT CGGGAAGAAA TTGGAATGGA ATAATATAGA TTCAATACAGA
4151 GAAAAAGGTT CTCTATTGAT GCAAACGCTG TACCTAGAGG ATAGGGATAG
4201 AGGAAGAGGG AAAATCGAA ATGAAAATAA TAAGAATAA AGCAAAAAAA
4251 AAATAAGTCG AAGATAGAAG AGCCCGAGATT CCAAAATGAAG AAATGGAAAC
4301 TCGAAAAGGA TCCTCTGAT TCTCAAAGAA TGAGGGGCAA GGGGATTGAT
4351 ACCGAGAAAAG ATTTCTCTT ATTATAAGAC GTGATTTGAT CCGCATATGT
4401 TTGGTAAAAG AACAAATCTTC TCCCTTAATC ATAAATGGAA AGTGTTCAT
4451 TAGAACATGA AAACGTGACT CAATTGGTCT TAGTTAGTCT TCGGGACGGA
4501 GTGGAAAGAAA GGGCGAAGAC TCTCGAACGA GGAAAAGGAT CCCTTCGAAA
4551 GAATTGAACG AGGAGCCGTA TTAGGTGAAA ATCTCATGTA CGATTCTGTA
4601 GAGGGACAGG AAGGGTGAAT TATCTGTGCA CTTTTCCACT ATCAACCCCA
4651 AAAAACCCAA CTCTGCCTTA C

Rice Right targeting sequence add

125878

Figure 33B

pMSK49.seq Length: 5263

Figure 34A

122488

1 GGGAACGGAT TCACCGCCGT ATGGCTGACC GGGGATTACT AGCGATTCC
 51 GCTTCATGCA GCGAGTTGC AGCCTGCAAT CGAACGTGAG GACGGGTTT
 101 TGGAGTTAGC TCACCCCTCGC GAGATCGCGA CCCTTGTCC CGCCCATG
 151 AGCACGTGTG TCGCCCCAGGG CATAAGGGC ATGATGACTT GGCTCATCC
 201 TCTCTTCTCCT CCGGCTTAAC ACCGGCGGTG TGTTCAAGGGT TCCAAACTCA
 251 TAGTGGGAAC TAAACACGAG GTTGCCTGCTC GTTGCAGAC TAAACCAAC
 301 ACCTTACGGC ACGAGCTGAC GACAGCCATG CACCACCTGT GTCCGCGTT
 351 CCGAGGGCAC CCTCTCTCTT CAAGAGGATT CGCGGATGT CAAGCCCTGG
 401 TAAGGTTCTT CGCTTTGCAT CGAATTAAAC CACATGCTCC ACCGCTTGTG
 451 CGGGCCCCCG TCAATTCTT TGAGTTTCAT TCTTGCGAAC GTACTCCCCA
 501 GGCGGGATAC TAAACGCGTT AGCTACAGCA CTGCACGGGT CGAGTCGAC
 551 AGCACCTAGT ATCCATCGTT TACGGCTAGG ACTACTGGGG TCTCTAATCC
 601 CATTTGCTCC CCTAGCTTC GTCTCTCAGT GTCAGTGTG GCCCAGCAGA
 651 GTGCTTCGC CGTGGTGTG CTTCCGATC TCAATGCATT TCACCGCTCC
 701 ACCGGAAATT CCTCTCTGCC CTACCGTACT CCAGCTTGGT AGTTTCCAC
 751 GCCTGTCCAG GGTIGAGCCC TGGGATTGAA CGCGGGACTT GAAAAGCCAC
 801 CTACAGACGC TTACGCCCCA ATCATTCCGG ATAACGCTTG CATCCTCTGT
 851 CTTACCGCGG CTGCTGGCAC AGAATTAGCC GATGCTTATT CCTCAGATA
 901 CGTCATTGTT TCTTCTCCGA GAAAAGAAGT TGACGACCCG TGGGCCTTCC
 951 ACCTCCACGC GGCAATTGCTC CGTCAGGCTT TCGCCATTG CGAAAATTG
 1001 CCCACGTGTG CCTCCCCGTAG GAGTCTGGGC CGTGTCTCAG TCCCAGTGTG
 1051 GCTGATCATC CTCTCGGACC AGCTACTGAT CATGCCCTTG GTAAGCTATT
 1101 GCCTCACCAA CTAGCTAAC AGACCGCGAGC CCCTCCTTGG GCGGATTCT
 1151 CTTTTGCTC CTCAAGCTAC GGGGTATTAG CAACCGTTTC CAGTTGTG
 1201 TCCCTCCCA AGGGCAGTTT CTTACGCGTT ACTCACCGT TCGCCACTGG
 1251 AAACACCACT TCCCGTTCCA CTTGCATGTG TTAAGCATGC CGCCAGCGTT
 1301 CATCCTGAGC CAGGATCGAA CTCTCCATGA GATTCATAGT TGCAATTACT
 1351 ATAGCTTCCT TATTCTTASA CAAAGCGGGAT TCAGGAATTGT CTTTCTTCC
 1401 AAGGATAACT TGTATCCAATG CGCTTCAGAT TATTAGCTTG GAGTTCGCCA
 1451 CCAGCAGTAT AGCCAACCC ACCCTATCAC GTCAATCCCA CAAGCCTCTT
 1501 ATCCATTCCC GTTCGATCGT GGCGGGGGGA GTAAGTCAAA ATAGAAAAAA
 1551 CTCACATTGG GTTGTAGGGAT AATCAAGGCTC GAACTGATGA CTTCCACCAC
 1601 GTCAAGGTGA CACTCTACCG CTGAGTTATA TCCCTTCCCC GTCCCTCGA
 1651 GAAAGAGAAT TACCGAATCC TAAGGCAAAG GGGCGAGAAA CTCAAGGCCA
 1701 CCCTTCTTCC GGGCTTTCTT TCCACACTAT TATGGATAGT CAAATAATGG
 1751 GAAAATTGG ATTCAATTGT CAACCGGTCC TATCGAAAAT AGGATTGACT
 1801 ATGGATTGCA GCATAGCAC ATGGTTTCAT AAAATCTGTA CGATTTTCCC
 1851 GATCTAAATC GAGCAGGTTT CCATGAAGAA gatcgacggg atcgataagc
 1901 tttCANGAAT AAATGCAAGA AAATAACCTC TCCCTCTTT TCTATAATGT
 1951 AAAACAAAAA GTCTATGTAA GTAAAATAC AGTAAATAAA TAAAAAGAAA
 2001 AAAAGAAAGG AGCAATAGCA CCCTCTTGTAG AGAACAAAGAA AATGATTATT
 2051 GCTCCCTTCTT TTTCAABACC TCCTATAGAC TAGGCCAGGA TCGCTCTAGA
 2101 gcTTATTTG TATAGTTCAT CCATGCCATG TGTAATCCCA GCAGCTGTTA
 2151 CAAACCTCAAG AAGGACCATG TGGCTCTCTC TTTCGTTGGG ATCTTTCGAA
 2201 AGGGCAGATT GTGTGGACAG GTAAATGGTTG TCTGGTAAAA GGACAGGGCC
 2251 ATCGCCAATT GGAGTATTGT GTTGATAATG GTCTGCTAGT TGAACGCTTC
 2301 CATCTTCAAT GTTGTGTCTA ATTTGAAGT TAGCTTGTAT TCCATTCTT
 2351 TGTTTGTCTG CGGTGATGTA TACGGTGTGG GAGTTGTAGT TGTAATTCCAA
 2401 CTTGTGGCCG AGGATGTTTC CGTCCTCTT GAAATCGATT CCCTTAAGCT
 2451 CGATCCTGTT GACGAGGGTG TCTCCCTCAA ACTTGACTTC AGCACGTGTC
 2501 TTGTAGTTCC CGTCGTCTT GAAAGAGATG GTCCCTCTCT GCACGTATCC
 2551 CTCAGGGCATG GCGCTCTTGA AGAAGTCGTG CCGCTTCATA TGATCTGGGT
 2601 ATCTTGAAA GAATTGAACA CCATAAGAGA AAGTAGTGAC AAGTGTGAC
 2651 CAAGGAACAG GTAGTTTCC AGTAGTGCAAA ATAAATTTAA GGGTAAGTTT
 2701 TCCGTATGTT GCATCACCTT CACCTCTCTCC ACTGACAGAA AATTGTGCC

Rice left targeting sequence

7/5/94

gfp

09/762105
PCT/US99/T7806

Figure 34B

pMSK49.seq Length: 5263

2751 CATTAAACATC ACCATCTAAT TCAACAAAGAA TTGGGACAAC TCCAGTGAAA
2801 AGTTCTTCTC CTTTACTggc CATggcgacc tccaaatttc cttcaactgc
2851 aagttctttg CCCACTACCT TGGGATCTC GCCTTCACG TAGTGGACAA
2901 ATTCTTCAA CTGATCTGG CGCGAGGCCA AGCGATCTC TTCTTGTC
2951 AGATAAGCCT GTCTAGCTTC AAGTATGACG GGCTGATACT GGGCCGGCAG
3001 GCGCTCATT GCCCAGTCGG CAGGCACATC CTTCGGCGC ATTTTGC
3051 TTACTGGCT GTACCAAAATG CGGGACAACG TAAGCACTAC ATTCGCTCA
3101 TCGCCAGCCC AGTCGGGCGG CGAGTTCAT AGCGTTAAGG TTTCATTAG
3151 CGCCTCAAAT AGATCCTGTT CAGGAACCGG ATCAAAGAGT TCCTCCG
3201 C1GGACCTAC CAAGGCAACG CTATGTTCTC TTGCTTTGT CAGCAAGATA
3251 GCCAGATCAA TGTCGATCGT GGCTGGCTCG AAGATACTG CAAAGATG
3301 ATTGCGTGC CATTCTCAA ATTGCACTTC GCGCTTAGCT GGATAACGCC
3351 ACGBAATGAT GTCGTCGTGC ACAACAAATGG TGACTCTAC AGCGCGGAGA
3401 ATCTCGCTCT CTCCAGGGGA AGCCGAAGTT TCCAAAAGGT CGTTGATCAA
3451 AGCTCGCCGC GTGTTTCTAT CAAGCCTTAC GGTCAACCGTA ACCAGCAAAT
3501 CAATATCACT GTGTGGCTTC AGGCCGCCAT CCACTGCGGA GCGGTACAAA
3551 TGTACGGCCA GCAACGTCGG TTGGAGATGG CGCTCGATGA CGCCAAC
3601 CTTCTGATAGT TGAGTCGATA CTTGGCGAT CACCGCTTCgt ctaggcaagt
3651 CTTCTTcaga aatgagttt tggtcgctag CTTGTCACC AGTCATGCTt
3701 GCCATATGTA TATCTCCCTC TTAAGTTAA ACAAAATTAT TTCTAGtGGG
3751 AAACCGTTGT GGTCTCCCTC CCAGAAATAT AGCCATCCCT GCCCCCTCAC
3801 GTCAATCCCCA CGAGCCTCTT ATCCATTCTC ATTGAACGAC GGCGGGGGAG
3851 C gagctcgaa ttccctgcggc cggatcTTAC CATTTCGAA GGAACGGGG
3901 CTACATTCTC TTTCATTTC CATTCAAGAG TTTCTTATCT GTTTCACGC
3951 CCTTTTTTGA GACCTCGAAA CATGAAATGG ACAAAATTCT TCTCTTAGGA
4001 ACACATACAA GAAAAAGGAT AATGGTAGCC CTCCCATTAA CTACTTCATT
4051 TCATTTATGA ATTTCATAGT AATAGAAATC CATGTCCTAC CGAGACAGAA
4101 TTTCGAACTT GCTATCCTCT TGCCATTAG GCAAAGATTG ACCTCTGTAG
4151 AAAGAATGAT TCATTGGAT CGATATGAGG ACCCAACTAC GTTGCATTGC
4201 AGAATCCATG TTCCATATT GAAAGGGTT GAACCTCTGTG CTCTCTCAT
4251 GGTACAAATCC TCTTCCTGCT GAGCCCCCTT TCTCTCGGT CCACAGAGAA
4301 AAAATGGAGG ACTGGTGCCT ACAGTTCATC ACGGAAGAAA GAACTCACAG
4351 AGCCGGGATC GCTAACTAAT AGAATAGTAC TACTAACTAA TACTAATATA
4401 TAGAAAATAGA TATctagcta gAAATAGAAA CAACTAATAT ATAGATAATC
4451 GAAATTGAAA AGAACTGTCT TTTCTGTATA CTTCCCCST TCTATTGCTA
4501 CCGCGGGTCT TATGCAATCG ATCGGATCAT ATAGATATCC CTTCAACACA
4551 ACATAGGTCA TCGAAAGGAT CTGGACGAC TCACCAAAGC ACGAAAGCCA
4601 GTTAGAAAAT GGATTCTTAT TTGAAGAGTG CCTAACCGCA TGGATAAGCT
4651 CACATTAAAC CGTCAATTG GGATCCAATT CGGGATTTTT CTTGGGAAGT
4701 TTCGGGAAGA ATTGGAAATG GAATAATATA GATTCTACACA GAGGAAAGG
4751 TTCTCTATTG ATGCAAACGC TGTACCTAGA GGATAGGGAT AGAGGAAGAG
4801 GGAAAATCG AAATGAAATA AATAAAGAAT AAAGCAAAAA AAAAATAAGT
4851 CGAAGATAGA AGAGCCCCAGA TTCCAAATGA AGAAATGGAA ACTCGAAAAG
4901 GATCCTTCTG ATTCTCAAAG AATGAGGGGC AAGGGATTG ATACCGAGAA
4951 AGATTCTTC TTATTATAAG ACGTGATTG ATCCGATAT GTTTGGTAAA
5001 AGAACAAATCT TCTCCTTAA TCATAAATGG AAAGTGTCA ATTAGAACAT
5051 GAAAACGTGA CTCAATTGGT CTTAGTTAGT CTTGGGACG GAGTGGAGA
5101 AAGGGCGAAG ACTCTCGAAC GAGGAAAAGG ATCCCTCGA AAGAATTGAA
5151 CGAGGAGCCG TATTAGGTGA AAATCTCATG TACGATTCTG TAGAGGGAC
5201 GGAAGGGTGA CTTATCTGTC GACTTTTCCA CTATCAACCC CAAAAAAACCC
5251 AACTCTGCCT TAC

Rice Right targeting sequence

Gene	Product	Plasmid
<i>aadA16gfp</i>	FLARE16-S	pMSK51 (BS)
<i>aadA16gfp-S1</i>	FLARE16-S1	pMSK56 (Nt-pRV111B)
<i>aadA16gfp-S2</i>	FLARE16-S2	pMSK57 (Nt-pRV111B)
<i>aadA11gfp-S3</i>	FLARE11-S3	pMSK49 (Os-pMSK49)

Figure 35